

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 19, 2005, 12:31:50 ; Search time 110 seconds
(without alignments)

889.156 Million cell updates/sec

Title: US-10-770-117-4

Perfect score: 1040

Sequence: 1 MSTNPKPKQKNKENTNRPO.....CSPSIFLLALLSLCTVPASA 191

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1040	100.0	3011	1	P26664 h genome po
2	1031	99.1	191	2	Q68113 hepatitis c
3	1031	99.1	191	2	Q68123 hepatitis c
4	1031	99.1	191	2	Q68124 hepatitis c
5	1031	99.1	191	2	Q68139 hepatitis c
6	1031	99.1	191	2	Q68149 hepatitis c
7	1031	99.1	191	2	Q6QY91 hepatitis c
8	1031	99.1	191	2	Q6QY92 hepatitis c
9	1031	99.1	191	2	Q6QY99 hepatitis c
10	1031	99.1	191	2	Q6QY91 hepatitis c
11	1031	99.1	191	2	Q6QY92 hepatitis c
12	1031	99.1	191	2	Q6QY96 hepatitis c
13	1031	99.1	191	2	Q6QY97 hepatitis c
14	1031	99.1	191	2	Q6QY98 hepatitis c
15	1031	99.1	191	2	Q6QY99 hepatitis c
16	1031	99.1	191	2	Q6QY91 hepatitis c
17	1031	99.1	191	2	Q6QY92 hepatitis c
18	1031	99.1	191	2	Q6QY96 hepatitis c
19	1031	99.1	191	2	Q6QY97 hepatitis c
20	1031	99.1	191	2	Q6QY98 hepatitis c
21	1031	99.1	191	2	Q6QY99 hepatitis c
22	1031	99.1	191	2	Q6QY91 hepatitis c
23	1031	99.1	191	2	Q6QY92 hepatitis c
24	1031	99.1	191	2	Q6QY96 hepatitis c
25	1031	99.1	191	2	Q6QY97 hepatitis c
26	1031	99.1	191	2	Q6QY98 hepatitis c
27	1031	99.1	191	2	Q6QY99 hepatitis c
28	1031	99.1	191	2	Q6QY91 hepatitis c
29	1031	99.1	191	2	Q6QY92 hepatitis c
30	1031	99.1	191	2	Q6QY96 hepatitis c
31	1031	99.1	191	2	Q6QY97 hepatitis c

Q6QYf6 hepatitis c
Q6QYf7 hepatitis c
Q6QYf9 hepatitis c
Q6QYg0 hepatitis c
Q6QYg5 hepatitis c
Q6QYj7 hepatitis c
Q6QYj9 hepatitis c
Q6QYk0 hepatitis c
Q6QYk2 hepatitis c
Q6QYk3 hepatitis c
Q6QYk6 hepatitis c
Q6QYk7 hepatitis c
Q6QYk8 hepatitis c
Q6QYk9 hepatitis c

ALIGNMENTS

RESULT 1
POLG_HCV1
ID_POLG_HCV1 STANDARD; PRT; 3011 AA.
AC P26664;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Genome polyprotein [Contains: Capsid protein C (Core protein) (P22); Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21) (P21) (P21); Protease/helicase NS3 (P70) (Hepacivirin) (EC 3.4.22.-); Nonstructural protein NS4A (P56); Nonstructural protein NS5A (P56); Nonstructural protein NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
DE Hepatitis C virus (isolate 1) (HCV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11104;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91172826; PubMed=1848704;
RA Choo Q.-L., Richman K.H., Han J.H., Berger K., Lee C., Dong C., Gallegos C., Coit D., Medina-Selby A., Barr P.J., Weiner A.J., Bradley D.W., Kuo G., Houghton M.;
RT "Genetic organization and diversity of the hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:2451-2455(1991).
CC -I- FUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are hydrophobic, suggesting a possible membrane-related function. NS3 and NS5 may play a role in the viral RNA replication.
CC -I- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral precursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'.
CC -I- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + (RNA) (N).
CC -I- SUBUNIT: The virion of this virus is a nucleocapsid covered by a lipoprotein envelope. The envelope consists of two proteins: protein M and glycoprotein E. The nucleocapsid is a complex of protein C and mRNA.
CC -I- SIMILARITY: Contains 1 peptidase S29 domain.
CC -I- SIMILARITY: Contains 1 peptidase U39 domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL: M62321; AAA45676.1; -.
DR PIR: A39166; GNWVC3
DR PDB: 1HEI; X-ray; A/B-1206-1656.
DR PDB: 1ONB; NMR; A-1349-1507.
DR MEROPS; S29.001; -.

[illegible]

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RX MEDLINE=94336721; PubMed=8058787;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the core gene of 14 hepatitis C virus
RL Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93376778; PubMed=8396266;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "At least 12 genotypes of hepatitis C virus predicted by sequence
RL analysis of the putative E1 gene of isolates collected worldwide.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8234-8238(1993).
DR EMBL; U10207; AAA21046.1; -.
DR PIR; PQ0804; PQ0804.
DR HSP; Q8Y51; ICWX.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR Polyprotein.
DR CHAIN 1 >191 core protein.
FT NON TER 191
FT CHAIN 191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 99.1%; Score 1031; DB 2; Length 191;
Best Local Similarity 99.0%; Pred. No. 2e-79;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKPKKNTNRPPQDVKFPGGQIVGGVLLPRGRLGVRAATKTSERSQPRG 60
DB 1 MSTNPKPKKNTNRPPQDVKFPGGQIVGGVLLPRGRLGVRAATKTSERSQPRG 60
QY 61 RRQIPKARRPEGRTPWAQPGYPWPLYGNECGWAGLLSPRGRSPSWGPTDPRRSRNLG 120
DB 61 RRQIPKARRPEGRTPWAQPGYPWPLYGNECGWAGLLSPRGRSPSWGPTDPRRSRNLG 120
QY 121 KVDTLTTCGFADLMGYIPLVGAPLGGAAALAHGVRVLEEDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVDTLTTCGFADLMGYIPLVGAPLGGAAALAHGVRVLEEDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191

RESULT 5
Q68139 PRELIMINARY; PRT; 191 AA.
AC Q68139
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94336721; PubMed=8058787;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the core gene of 14 hepatitis C virus
RL Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994).
RN [2]

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RP SEQUENCE FROM N.A.
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93376778; PubMed=8396266;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "At least 12 genotypes of hepatitis C virus predicted by sequence
RL analysis of the putative E1 gene of isolates collected worldwide.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8234-8238(1993).
DR EMBL; U10222; AAA21061.1; -.
DR PIR; PQ0804; PQ0804.
DR HSP; Q8Y51; ICWX.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR Polyprotein.
DR CHAIN 1 >191 core protein.
FT NON TER 191
FT CHAIN 191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 99.1%; Score 1031; DB 2; Length 191;
Best Local Similarity 99.0%; Pred. No. 2e-79;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKPKKNTNRPPQDVKFPGGQIVGGVLLPRGRLGVRAATKTSERSQPRG 60
DB 1 MSTNPKPKKNTNRPPQDVKFPGGQIVGGVLLPRGRLGVRAATKTSERSQPRG 60
QY 61 RRQIPKARRPEGRTPWAQPGYPWPLYGNECGWAGLLSPRGRSPSWGPTDPRRSRNLG 120
DB 61 RRQIPKARRPEGRTPWAQPGYPWPLYGNECGWAGLLSPRGRSPSWGPTDPRRSRNLG 120
QY 121 KVDTLTTCGFADLMGYIPLVGAPLGGAAALAHGVRVLEEDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVDTLTTCGFADLMGYIPLVGAPLGGAAALAHGVRVLEEDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191

RESULT 6
Q68149 PRELIMINARY; PRT; 191 AA.
AC Q68149
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94336721; PubMed=8058787;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the core gene of 14 hepatitis C virus
RL Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
RN [3]

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OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sherman K.E., Qin H., Shire N., Rouster S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY522318; AAS15480.1; -
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV core; 1.
FT NON_TER 191_191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 99.1%; Score 1031; DB 2; Length 191;
Best Local Similarity 99.0%; Pred. No. 2e-79;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSTNPKPKKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db [1]
1 MSTNPKPQKTKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60

Qy 61 RRQIPKARRPEGRTWAGPGYWPPLYGNECGWAGWLLSPRGRSPSWGPTDPRRSRNLG 120
Db [1]
61 RRQIPKARRPEGRTWAGPGYWPPLYGNECGWAGWLLSPRGRSPSWGPTDPRRSRNLG 120

Qy 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db [1]
121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db [1]
181 LLSCLTVPASA 191

RESULT 10
Q6QYAL ID Q6QYAL PRELIMINARY; PRT; 191 AA.
AC Q6QYAL;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sherman K.E., Qin H., Shire N., Rouster S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY522318; AAS15478.1; -
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV core; 1.
FT NON_TER 191_191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 99.1%; Score 1031; DB 2; Length 191;
Best Local Similarity 99.0%; Pred. No. 2e-79;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSTNPKPKKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db [1]
1 MSTNPKPQKTKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60

Qy 61 RRQIPKARRPEGRTWAGPGYWPPLYGNECGWAGWLLSPRGRSPSWGPTDPRRSRNLG 120
Db [1]
61 RRQIPKARRPEGRTWAGPGYWPPLYGNECGWAGWLLSPRGRSPSWGPTDPRRSRNLG 120

Qy 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db [1]
121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db [1]
181 LLSCLTVPASA 191

RESULT 10
Q6QYAL ID Q6QYAL PRELIMINARY; PRT; 191 AA.
AC Q6QYAL;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sherman K.E., Qin H., Shire N., Rouster S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY522316; AAS15478.1; -
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV core; 1.
FT NON_TER 191_191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 99.1%; Score 1031; DB 2; Length 191;
Best Local Similarity 99.0%; Pred. No. 2e-79;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSTNPKPKKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db [1]
1 MSTNPKPQKTKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60

Qy 61 RRQIPKARRPEGRTWAGPGYWPPLYGNECGWAGWLLSPRGRSPSWGPTDPRRSRNLG 120
Db [1]
61 RRQIPKARRPEGRTWAGPGYWPPLYGNECGWAGWLLSPRGRSPSWGPTDPRRSRNLG 120
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Qy 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db [1]
121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db [1]
181 LLSCLTVPASA 191

RESULT 11
Q6QYAL ID Q6QYAL PRELIMINARY; PRT; 191 AA.
AC Q6QYAL;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sherman K.E., Qin H., Shire N., Rouster S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY522315; AAS15477.1; -
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV core; 1.
FT NON_TER 191_191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 99.1%; Score 1031; DB 2; Length 191;
Best Local Similarity 99.0%; Pred. No. 2e-79;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSTNPKPKKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db [1]
1 MSTNPKPQKTKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60

Qy 61 RRQIPKARRPEGRTWAGPGYWPPLYGNECGWAGWLLSPRGRSPSWGPTDPRRSRNLG 120
Db [1]
61 RRQIPKARRPEGRTWAGPGYWPPLYGNECGWAGWLLSPRGRSPSWGPTDPRRSRNLG 120

Qy 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db [1]
121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db [1]
181 LLSCLTVPASA 191

RESULT 12
Q6QYAL ID Q6QYAL PRELIMINARY; PRT; 191 AA.
AC Q6QYAL;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sherman K.E., Qin H., Shire N., Rouster S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY522311; AAS15473.1; -;
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
FT NON TER 191_191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 99.1%; Score 1031; DB 2; Length 191;
Best Local Similarity 99.0%; Pred. No. 2e-79;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNRTNRPPQDVKPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKPQKTKRNTNRPPQDVKPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60

Qy 61 RRQIPKARRPEGRGTWAQPGYPWPLYNGEGCGWAGLLSPRGSPSWGPTDPRRSRNLG 120
Db 61 RRQIPKARRPEGRGTWAQPGYPWPLYNGEGCGWAGLLSPRGSPSWGPTDPRRSRNLG 120

Qy 121 KVDTLTTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180
Db 121 KVDTLTTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 13
Q6QYA7 PRELIMINARY; PRT; 191 AA.
AC Q6QYA7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sherman K.E., Qin H., Shire N., Rouster S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY522310; AAS15472.1; -;
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
FT NON TER 191_191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 99.1%; Score 1031; DB 2; Length 191;
Best Local Similarity 99.0%; Pred. No. 2e-79;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNRTNRPPQDVKPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKPQKTKRNTNRPPQDVKPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60

Qy 61 RRQIPKARRPEGRGTWAQPGYPWPLYNGEGCGWAGLLSPRGSPSWGPTDPRRSRNLG 120
Db 61 RRQIPKARRPEGRGTWAQPGYPWPLYNGEGCGWAGLLSPRGSPSWGPTDPRRSRNLG 120

Qy 121 KVDTLTTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180
Db 121 KVDTLTTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 14
Q6QYB1 PRELIMINARY; PRT; 191 AA.
AC Q6QYB1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sherman K.E., Qin H., Shire N., Rouster S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY522306; AAS15468.1; -;
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
FT NON TER 191_191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 99.1%; Score 1031; DB 2; Length 191;
Best Local Similarity 99.0%; Pred. No. 2e-79;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNRTNRPPQDVKPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKPQKTKRNTNRPPQDVKPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60

Qy 61 RRQIPKARRPEGRGTWAQPGYPWPLYNGEGCGWAGLLSPRGSPSWGPTDPRRSRNLG 120
Db 61 RRQIPKARRPEGRGTWAQPGYPWPLYNGEGCGWAGLLSPRGSPSWGPTDPRRSRNLG 120

Qy 121 KVDTLTTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180
Db 121 KVDTLTTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 15
Q6QYB2 PRELIMINARY; PRT; 191 AA.
AC Q6QYB2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sherman K.E., Qin H., Shire N., Rouster S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY522305; AAS15467.1; -;
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
```

DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
FT NON_TER 191_191
SQ SEQUENCE 191 AA; 20766 MW;

Query Match	99.1%;	Score 1031;	DB 2;	Length 191;
Best Local Similarity	99.0%;	Pred. No. 2e-79;		
Matches 189;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	MSTNPKQKKNKRNTRRRPQDVKEPFGGQIVGGVYLLPRRGLRGVRAKTRKTSERS	PRG 60	
Db	1	MSTNPKQKRTKRNTRRRPQDVKEPFGGQIVGGVYLLPRRGLRGVRAKTRKTSERS	PRG 60	
Qy	61	RRQIPKARRPEGRWTAAQGPYPWPLYNKGCGGAGWLLSPRGSPPSGWGTDPDRRSRN	NLG 120	
Db	61	RRQIPKARRPEGRWTAAQGPYPWPLYNKGCGGAGWLLSPRGSPPSGWGTDPDRRSRN	NLG 120	
Qy	121	KVIDTLTCGFPADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNVTATGNLPCCSFSI	FLLA 180	
Db	121	KVIDTLTCGFPADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNVTATGNLPCCSFSI	FLLA 180	
Qy	181	LLSCLTVPASA	191	
Db	181	LLSCLTVPASA	191	

Search completed: August 19, 2005, 12:43:13
Job time : 111 secs

Dn	1	MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG	60
Qy	61	RRQPIKARRPEGRWTAQPGYPWPPLYGNECGWAGWLLSPRGRPSWGPTDPRRRRNLG	120
Dn	61	RRQPIKARRPEGRWTAQPGYPWPPLYGNECGWAGWLLSPRGRPSWGPTDPRRRRNLG	120
Qy	121	KVIDTLTCGFADLMGYIPLVGAALAHGVRLVDGVNYYATGNLPGCSFSIFLLA	180
Dn	121	KVIDTLTCGFADLMGYIPLVGAALAHGVRLVDGVNYYATGNLPGCSFSIFLLA	180
Qy	181	LLSCLTVPASA	191
Dn	181	LLSCLTVPASA	191
RESULT 2			
GNWVCJ			
genome polyprotein - hepatitis C virus (strain H)			
N;Contains: capsid protein C; envelope protein M; hepatitis C virus (strain H)			
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5			
C;Species: hepatitis C virus			
A;Note: host Homo sapiens (man)			
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004			
A;Accession: A36814; A41546			
submitted to GenBank, July 1992			
A;Description: Genomic structure of the human prototype strain H of hepatitis C virus: C			
A;Reference number: A36814			
A;Accession: A36814			
A;Molecule type: genomic RNA			
A;Residues: 1-3011 <NC>			
A;Cross-references: UNIPROT:P27958; GB:M67463; NID:G329737; PIDN:AAA45534.1; PID:G329738			
R;Inchauspe, G.; Zebadee, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.			
Proc. Natl. Acad. Sci. U.S.A. 88, 10292-10296, 1991			
A;Title: Genomic structure of the human prototype strain H of hepatitis C virus: compar			
A;Reference number: A41546; MUID:920522256; PMID:1658800			
A;Contents: annotation			
A;Note: neither amino acid nor nucleotide sequence is given			
C;Superfamily: hepatitis C virus genome polyprotein			
C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructura			
F;1-115/Product: capsid protein C #status predicted <CPC>			
F;116-191/Product: envelope protein M #status predicted <EPW>			
F;192-389/Product: major envelope protein E #status predicted <MEE>			
F;390-729/Product: nonstructural protein NS1 #status predicted <NS1>			
F;730-1006/Product: nonstructural protein NS2 #status predicted <NS2>			
F;1007-1615/Product: hepatitis C virus #status predicted <NS3>			
F;1230-1237/Region: nucleotide-binding motif A (P-loop)			
F;1312-1317/Region: nucleotide-binding motif B			
F;1316-1319/Region: DEXH motif			
F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>			
F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>			
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>			
F;196, 209, 234, 305, 325, 417, 423, 430, 448, 476, 532, 540, 556, 576, 623, 645, 1213, 1255, 2041, 2240, 23			
Query Match 99.1%; Score 1031; DB 1; Length 3011;			
Best Local Similarity 99.0%; Pred. No. 4.8e-77;			
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
Qy	1	MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG	60
Dn	1	MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG	60
Qy	61	RRQPIKARRPEGRWTAQPGYPWPPLYGNECGWAGWLLSPRGRPSWGPTDPRRRRNLG	120
Dn	61	RRQPIKARRPEGRWTAQPGYPWPPLYGNECGWAGWLLSPRGRPSWGPTDPRRRRNLG	120
Qy	121	KVIDTLTCGFADLMGYIPLVGAALAHGVRLVDGVNYYATGNLPGCSFSIFLLA	180
Dn	121	KVIDTLTCGFADLMGYIPLVGAALAHGVRLVDGVNYYATGNLPGCSFSIFLLA	180
Qy	181	LLSCLTVPASA	191
Dn	181	LLSCLTVPASA	191

RESULT 3			
GNWVCJ			
genome polyprotein - hepatitis C virus (strain J)			
N;Contains: capsid protein C; envelope protein M; major envelope protein E; nonstructural			
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5			
C;Species: hepatitis C virus			
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004			
A;Accession: A39253; PS0086			
R;Kato, N.; Hijikata, M.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Sugimura, T.; Shimoto			
Proc. Natl. Acad. Sci. U.S.A. 87, 9524-9528, 1990			
A;Title: Molecular cloning of the human hepatitis C virus genome from Japanese patients v			
A;Reference number: A39253; MUID:91088550; PMID:2175903			
A;Accession: A39253			
A;Molecule type: Genomic RNA			
A;Residues: 1-3010 <KAT>			
A;Cross-references: UNIPROT:P26662; GB:D90208; NID:G221610; PIDN:BAA14233.1; PID:G221611			
R;Kato, N.; Ohkoshi, S.; Shimotohno, K.			
Proc. Jpn. Acad. 65B, 219-223, 1989			
A;Title: Japanese isolates of the non-A, non-B hepatitis viral genome show sequence vari			
A;Reference number: PS0085			
A;Accession: PS0086			
A;Molecule type: genomic RNA			
A;Residues: 2650-2707 <KA2>			
A;Experimental source: Japanese isolate			
C;Comment: The cleavage sites of this polyprotein have not been determined.			
C;Superfamily: hepatitis C virus genome polyprotein			
C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serine			
F;2-115/Product: capsid protein C #status predicted <CPC>			
F;116-191/Product: envelope protein M #status predicted <EPW>			
F;192-389/Product: major envelope protein E #status predicted <MEE>			
F;390-729/Product: nonstructural protein NS1 #status predicted <NS1>			
F;730-1006/Product: nonstructural protein NS2 #status predicted <NS2>			
F;1007-1615/Product: hepatitis C virus #status predicted <NS3>			
F;1230-1237/Region: nucleotide-binding motif A (P-loop)			
F;1312-1317/Region: nucleotide-binding motif B			
F;1316-1319/Region: DEXH motif			
F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>			
F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>			
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>			
F;196, 209, 234, 305, 325, 417, 423, 430, 448, 532, 556, 576, 623, 645, 1213, 1255, 2041, 2077, 2240, 2;			
Query Match 98.1%; Score 1020; DB 1; Length 3010;			
Best Local Similarity 97.9%; Pred. No. 3.9e-76;			
Matches 187; Conservative 2; Mismatches 2; Indels 0; Gaps 0;			
Qy	1	MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG	60
Dn	1	MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG	60
Qy	61	RRQPIKARRPEGRWTAQPGYPWPPLYGNECGWAGWLLSPRGRPSWGPTDPRRRRNLG	120
Dn	61	RRQPIKARRPEGRWTAQPGYPWPPLYGNECGWAGWLLSPRGRPSWGPTDPRRRRNLG	120
Qy	121	KVIDTLTCGFADLMGYIPLVGAALAHGVRLVDGVNYYATGNLPGCSFSIFLLA	180
Dn	121	KVIDTLTCGFADLMGYIPLVGAALAHGVRLVDGVNYYATGNLPGCSFSIFLLA	180
Qy	181	LLSCLTVPASA	191
Dn	181	LLSCLTVPASA	191
RESULT 4			
S40770			
genome polyprotein - hepatitis C virus			
N;Contains: capsid protein C; envelope protein M; hepatitis C virus (strain H)			
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5			
C;Species: hepatitis C virus			
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004			
A;Accession: S40770; PC1285			
R;Okamoto, H.			

submitted to the EMBL Data Library, March 1992

A;Reference number: S40770
A;Accession: S40770
A;Molecule type: genomic RNA
A;Residues: 1-3011 <OK>
A;Cross-references: UNIPROT:Q03463; EMBL:D10749; NID:g221586; PIDN:BAA01582.1; PID:g221586
R;Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Yoshizawa, H.; Tsuda, Jpn. J. Exp. Med. 60, 167-177, 1990

A;Title: The 5'-terminal sequence of the hepatitis C virus genome.

A;Reference number: PC1284; MUID:91013116; PMID:2170712

A;Accession: PC1285

A;Molecule type: genomic RNA

A;Residues: 1-513 <OK2>

A;Cross-references: GB:D00831; NID:g221511; PIDN:BAA00705.1; PID:g221512

A;Experimental source: isolate HC-J1

C;Superfamily: hepatitis C virus genome polypeptide

C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polypeptide; serine

F;2-115/Product: capsid protein C #status predicted <CPC>

F;116-191/Product: envelope protein M #status predicted <EPM>

F;192-389/Product: major envelope protein E #status predicted <MEE>

F;390-729/Product: nonstructural protein NS1 #status predicted <NS1>

F;730-1006/Product: nonstructural protein NS2 #status predicted <NS2>

F;1007-1615/Product: hepatitis virus #status predicted <NS3>

F;1230-1237/Region: nucleotide-binding motif A (P-loop)

F;1312-1317/Region: nucleotide-binding motif B

F;1316-1319/Region: DEXH motif

F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>

F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>

F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>

Query Match 97.9%; Score 1018; DB 1; Length 3011;
Best Local Similarity 97.9%; Pred. No. 5.7e-76;
Matches 187; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSTNPKPKQKNTNRRPQDVKFGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

DB 1 MSTIPKQKNTNRRPQDVKFGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

QY 61 RRQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGRSPSGPTDPRRSNGLG 120

DB 61 RRQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGRSPSGPTDPRRSNGLG 120

QY 121 KVIDTLTCGFADLMGYIPLVGAAPLGAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180

DB 121 KVIDTLTCGFADLMGYIPLVGAAPLGAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180

QY 181 LLSCLTVPASA 191

DB 181 LLSCLTVPASA 191

RESULT 5

JQ1584

genome polypeptide - hepatitis C virus (strain U.K.) (fragment)

N;Contains: core protein C; envelope protein E1; envelope protein E2; nonstructural protein

C;Species: hepatitis C virus

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C;Accession: JQ1584

R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.

J. Gen. Virol. 73, 1521-1525, 1992

A;Title: Cloning and sequencing of the structural region and expression of putative core

A;Reference number: JQ1584; MUID:92300349; PMID:1318944

A;Accession: JQ1584

A;Molecule type: genomic RNA

A;Residues: 1-640 <KUM>

A;Cross-references: UNIPROT:Q68966; GB:X84079; NID:g643119; PIDN:CAA58888.1; PID:g643120

C;Superfamily: hepatitis C virus genome polypeptide

C;Keywords: core protein; envelope protein; glycoprotein; nonstructural protein; polypeptide

F;1-191/Product: core protein C #status predicted <CPC>

F;192-389/Product: envelope protein E1 #status predicted <EE1>

F;390-640/Product: envelope protein E2 and nonstructural protein NS1 #status predicted <NS1>

F;196, 209, 234, 305, 417, 430, 448, 476, 540, 556, 576, 623/Binding site: carbohydrate (Asn) (cova

Query Match 97.7%; Score 1016; DB 2; Length 640;

Best Local Similarity 97.4%; Pred. No. 2e-76;

Matches 186; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSTNPKPKQKNTNRRPQDVKFGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

DB 1 MSTNPKPKQKNTNRRPQDVKFGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

QY 61 RRQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGRSPSGPTDPRRSNGLG 120

DB 61 RRQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGRSPSGPTDPRRSNGLG 120

QY 121 KVIDTLTCGFADLMGYIPLVGAAPLGAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180

DB 121 KVIDTLTCGFADLMGYIPLVGAAPLGAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180

QY 181 LLSCLTVPASA 191

DB 181 LLSCLTVPASA 191

RESULT 6

S12707

genome polypeptide - hepatitis C virus (fragment)

N;Contains: core protein; envelope protein

C;Species: hepatitis C virus

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: S12707

R;Takeuchi, K.; Kubo, Y.; Boonmar, S.; Watanabe, Y.; Katayama, T.; Choo, Q.L.; Kuo, G.;

Nucleic Acids Res. 18, 4626, 1990

A;Title: Nucleotide sequence of core and envelope genes of the hepatitis C virus genome

A;Reference number: S12707; MUID:90356432; PMID:2117749

A;Accession: S12707

A;Molecule type: genomic RNA

A;Residues: 1-441 <TAK>

A;Cross-references: UNIPROT:Q81776; EMBL:D00574; NID:g221656; PIDN:BAA00452.1; PID:g221656

C;Superfamily: hepatitis C virus genome polypeptide

C;Keywords: polypeptide

Query Match 97.6%; Score 1015; DB 2; Length 441;

Best Local Similarity 97.4%; Pred. No. 1.7e-76;

Matches 186; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSTNPKPKQKNTNRRPQDVKFGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

DB 1 MSTNPKPKQKNTNRRPQDVKFGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

QY 61 RRQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGRSPSGPTDPRRSNGLG 120

DB 61 RRQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGRSPSGPTDPRRSNGLG 120

QY 121 KVIDTLTCGFADLMGYIPLVGAAPLGAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180

DB 121 KVIDTLTCGFADLMGYIPLVGAAPLGAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180

QY 181 LLSCLTVPASA 191

DB 181 LLSCLTVPASA 191

RESULT 7

S32740

polypeptide - hepatitis C virus (isolate Russian) (fragment)

N;Contains: capsid protein C; envelope protein M

C;Species: hepatitis C virus

C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004

C;Accession: S32740

R;Vassiliev, V.B.; Vlazov, S.O.; Kotova, E.Y.; Nosikov, V.V.

submitted to the EMBL Data Library, April 1993

A;Description: Evidence of new HCV variant of European isolate in Russia.

A;Reference number: S32740

A;Accession: S32740

A;Molecule type: genomic RNA

A;Residues: 1-189 <VAS>
A;Cross-references: UNIPROT:Q68873; EMBL:X71407
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein; envelope protein; polyprotein
F;1-115/Product: capsid protein C #status predicted <CPC>
F;116-189/Product: envelope protein M #status predicted <EPM>

Query Match 97.5%; Score 1014; DB 2; Length 189;
Best Local Similarity 98.4%; Pred. No. 9.1e-77;
Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSTNPKPKKNTNRRPQDVKPPGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60
DB 1 MSTNPKPQRTKNTNRRPQDVKPPGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60

QY 61 RRQPIPKARPEGRTHAQCYPWPLYGNECGWAGLLSPRGRPSWGPDPDRRRSRNLG 120
DB 61 RRQPIPKARPEGRTHAQCYPWPLYGNECGWAGLLSPRGRPSWGPDPDRRRSRNLG 120

QY 121 KVIDTLTCGFADLMGYIPLVGAFLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPLVGAFLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

QY 181 LLSCLTVPASA 189
DB 181 LLSCLTVPASA 189

RESULT 8
S18031
genome polyprotein - hepatitis C virus (isolate JK2) (fragment)
N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C;Species: hepatitis C virus
A;Variety: isolate JK2
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
R;Honda, M.; Kaneko, S.; Maeaehi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus iso
A;Reference number: S18029
A;Accession: S18031
A;Molecule type: genomic RNA
A;Residues: 1-782 <HON>
A;Cross-references: UNIPROT:Q68950; EMBL:X61593
A;Experimental source: isolate JK2
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
F;1-191/Product: core protein #status predicted <MAT1>
F;192-383/Product: envelope protein 1 #status predicted <MAT2>
F;384-733/Product: NS1/E2 protein #status predicted <MAT3>
F;734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>

Query Match 97.2%; Score 1011; DB 2; Length 782;
Best Local Similarity 96.9%; Pred. No. 6.1e-76;
Matches 185; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSTNPKPKKNTNRRPQDVKPPGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60
DB 1 MSTNPKPQRTKNTNRRPQDVKPPGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60

QY 61 RRQPIPKARPEGRTHAQCYPWPLYGNECGWAGLLSPRGRPSWGPDPDRRRSRNLG 120
DB 61 RRQPIPKARPEGRTHAQCYPWPLYGNECGWAGLLSPRGRPSWGPDPDRRRSRNLG 120

QY 121 KVIDTLTCGFADLMGYIPLVGAFLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPLVGAFLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191

RESULT 9
PN0677
hypothetical protein 787 - hepatitis C virus (fragment)
C;Species: hepatitis C virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: PN0677
R;Cho, S.H.; Yoon, J.I.; Chang, J.E.; Ahn, B.M.; Lee, C.H.; Lee, Y.I.
Biochem. Biophys. Res. Commun. 196; 780-789, 1993
A;Title: Genomic typing of hepatitis C viruses from Korean patients: Implications of gen
C;Keywords: glycoprotein; nonstructural protein
F;196,209,234,250,305,325,421,427,452,536,544,560,580,627,649/Binding site: carbohydrate
A;Reference number: PN0677; MUID:94059104; PMID:8240354
A;Accession: PN0677
A;Molecule type: mRNA
A;Residues: 1-787 <CHO>
A;Cross-references: UNIPROT:Q08244; GB:L20498; NID:gl381031; PIDN:AAB02608.1; PID:gl38103
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: glycoprotein; nonstructural protein
F;196,209,234,250,305,325,421,427,452,536,544,560,580,627,649/Binding site: carbohydrate

Query Match 97.2%; Score 1011; DB 2; Length 787;
Best Local Similarity 96.9%; Pred. No. 6.1e-76;
Matches 185; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSTNPKPKKNTNRRPQDVKPPGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60
DB 1 MSTNPKPQRTKNTNRRPQDVKPPGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60

QY 61 RRQPIPKARPEGRTHAQCYPWPLYGNECGWAGLLSPRGRPSWGPDPDRRRSRNLG 120
DB 61 RRQPIPKARPEGRTHAQCYPWPLYGNECGWAGLLSPRGRPSWGPDPDRRRSRNLG 120

QY 121 KVIDTLTCGFADLMGYIPLVGAFLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPLVGAFLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191

RESULT 10
GNWVTC
genome polyprotein - hepatitis C virus
N;Contains: capsid protein C; envelope protein M; hepatitis C virus genome polyprotein
C;Species: hepatitis C virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: A38465
R;Takamizawa, A.; Mori, C.; Fuke, I.; Manabe, S.; Murakami, S.; Fujita, J.; Onishi, E.; I
J. Virol. 65; 1105-1113, 1991
A;Title: Structure and organization of the hepatitis C virus genome isolated from human
A;Reference number: A38465; MUID:91140698; PMID:1847440
A;Accession: A38465
A;Molecule type: genomic RNA
A;Residues: 1-3010 <TAK>
A;Cross-references: EMBL:M58335; NID:g329770; PIDN:AAA72945.1; PID:g3297;
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructural
F;2-115/Product: capsid protein C #status predicted <CPC>
F;116-191/Product: envelope protein M #status predicted <EPM>
F;192-389/Product: major envelope protein NS1 #status predicted <MEE>
F;390-729/Product: nonstructural protein NS2 #status predicted <NS1>
F;730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F;1007-1615/Product: hepatitis C virus genome polyprotein
F;1230-1237/Region: nucleotide-binding motif A (P-loop)
F;1312-1317/Region: nucleotide-binding motif B
F;1316-1319/Region: DEXH motif
F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,2077,224

Query Match 97.2%; Score 1011; DB 1; Length 3010;
Best Local Similarity 97.4%; Pred. No. 2.2e-75;

Matches 186; Conservative 1; Mismatches 4; Indels 0; Gaps 0;	
Qy	1 MSTNPKQKKNKNTNRRPQDVKFGGGQIVGGVYLLPRGPRGLGVRAATKTSERSQPRG 60 :
Db	1 MSTNPKPQKTKNTNRRPQDVKFGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60 :
Qy	61 RRQPIPKARRPEGRWTAAQPGYPWPLYGNECGWAGWLLSPRGRSPSGMPTDPRRRSRNLG 120 :
Db	61 RRQPIPKARRPEGRWTAAQPGYPWPLYGNEGLWAGWLLSPRGRSPSGMPTDPRRRSRNLG 120 :
Qy	121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180 :
Db	121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180 :
Qy	181 LLSCLTVPASA 191 :
Db	181 LLSCLTTPASA 191 :
RESULT 11	
PC1284	
genome polyprotein - hepatitis C virus (isolate HC-J4) (fragment)	
N;Contains: hepatitis C virus	
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004	
C;Accession: PC1284	
R;Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Yoshizawa, H.; Tauda, Jpn. J. Exp. Med. 60; 167-177, 1990	
A;Title: The 5'-terminal sequence of the hepatitis C virus genome.	
A;Reference number: PC1284; MUID:91013116; PMID:2170712	
A;Accession: PC1284	
A;Molecule type: genomic RNA	
A;Residues: 1-513 <OKA>	
A;Cross-references: UNIPROT:Q81221; GB:D00832; NID:g221513; PIDN:BAA00706.1; PID:g221514	
C;Superfamily: hepatitis C virus genome polyprotein	
Query Match 96.8%; Score 1007; DB 2; Length 513;	
Best Local Similarity 96.9%; Pred. No. 8.8e-76;	
Matches 185; Conservative 2; Mismatches 4; Indels 0; Gaps 0;	
Qy	1 MSTNPKQKKNKNTNRRPQDVKFGGGQIVGGVYLLPRGPRGLGVRAATKTSERSQPRG 60 :
Db	1 MSTNPKPQKTKNTNRRPQDVKFGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60 :
Qy	61 RRQPIPKARRPEGRWTAAQPGYPWPLYGNECGWAGWLLSPRGRSPSGMPTDPRRRSRNLG 120 :
Db	61 WRQPIPKARRPEGRWTAAQPGYPWPLYGNEGLWAGWLLSPRGRSPSGMPTDPRRRSRNLG 120 :
Qy	121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180 :
Db	121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180 :
Qy	181 LLSCLTVPASA 191 :
Db	181 LLSCLTTPASA 191 :
RESULT 12	
S21471	
genome polyprotein - hepatitis C virus (fragment)	
N;Contains: capsid protein; envelope protein	
C;Species: hepatitis C virus	
C;Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004	
C;Accession: S21471	
R;Mogam, W.K.	
A;Reference number: S21471	
A;Accession: S21471	
A;Molecule type: genomic RNA	
A;Residues: 1-369 <MOG>	
A;Cross-references: UNIPROT:Q68969; EMBL:X65924; NID:g59466; PIDN:CAA46717.1; PID:g59467	
C;Superfamily: hepatitis C virus genome polyprotein	
C;Keywords: capsid protein; envelope protein; glycoprotein; polyprotein	

Query Match 96.3%; Score 1002; DB 2; Length 369;	
Best Local Similarity 96.3%; Pred. No. 1.7e-75;	
Matches 184; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	
Qy	1 MSTNPKQKKNKNTNRRPQDVKFGGGQIVGGVYLLPRGPRGLGVRAATKTSERSQPRG 60 :
Db	1 MSTNPKPQKTKNTNRRPQDVKFGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60 :
Qy	61 RRQPIPKARRPEGRWTAAQPGYPWPLYGNECGWAGWLLSPRGRSPSGMPTDPRRRSRNLG 120 :
Db	61 RRQPIPKARRPEGRWTAAQPGYPWPLYGNEGLWAGWLLSPRGRSPSGMPTDPRRRSRNLG 120 :
Qy	121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180 :
Db	121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180 :
Qy	181 LLSCLTVPASA 191 :
Db	181 LLSCLTTPASA 191 :
RESULT 13	
S19876	
genome polyprotein - hepatitis C virus (isolate JKS) (fragment)	
N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein	
C;Species: hepatitis C virus	
A;Variety: isolate JKS	
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004	
C;Accession: S19876	
R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.	
submitted to the EMBL Data Library, September 1991	
A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus iso1	
A;Reference number: S18029	
A;Accession: S19876	
A;Molecule type: genomic RNA	
A;Residues: 1-782 <HON>	
A;Cross-references: UNIPROT:Q68953; EMBL:X61595; NID:g59486; PIDN:CAA43792.1; PID:g59487	
A;Superfamily: hepatitis C virus genome polyprotein	
C;Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural 1	
F;1-191/Product: core protein #status predicted <MAT1>	
F;192-383/Product: envelope protein 1 #status predicted <MAT2>	
F;384-733/Product: NS1/E2 protein #status predicted <MAT3>	
F;734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>	
Query Match 96.2%; Score 1000; DB 2; Length 782;	
Best Local Similarity 95.8%; Pred. No. 5e-75;	
Matches 183; Conservative 3; Mismatches 5; Indels 0; Gaps 0;	
Qy	1 MSTNPKQKKNKNTNRRPQDVKFGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60 :
Db	1 MSTNPKPQKTKNTNRRPQDVKFGGGQIVGGVYLLFRRGLGVRAATKTSERSQPRG 60 :
Qy	61 RRQPIPKARRPEGRWTAAQPGYPWPLYGNECGWAGWLLSPRGRSPSGMPTDPRRRSRNLG 120 :
Db	61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGLWAGWLLSPRGRSPSGMPTDPRRRSRNLG 120 :
Qy	121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180 :
Db	121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180 :
Qy	181 LLSCLTVPASA 191 :
Db	181 LLSCLTTPASA 191 :
RESULT 14	
A44150	
structural protein - hepatitis C virus	
C;Species: hepatitis C virus	
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004	
C;Accession: A44150	
R;Ching, W.M.; Wyckowski, C.; Beach, M.J.; Wang, H.; Davies, C.L.; Carl, M.; Bradley, D.	

Proc. Natl. Acad. Sci. U.S.A. 89, 3190-3194, 1992
A>Title: Interaction of immune sera with synthetic peptides corresponding to the structure of hepatitis C virus genome polyprotein
A;Reference number: A44150; MUID:92228749; PMID:1373489
A;Accession: A44150
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: genomic RNA
A;Residues: 1-513 <CHI>
A;Cross-references: UNIPROT:Q91FE5; UNIPROT:O36579; UNIPROT:O36610; UNIPROT:Q9ELS8; UNIPROT:Q9ELS9
C;Superfamily: hepatitis C virus genome polyprotein

Query Match 96.0%; Score 998; DB 2; Length 513;
Best Local Similarity 97.9%; Pred. No. 4.9e-75;
Matches 188; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 MSTNPKQKKNKNTNRPPQDVKPPGGQIVGGVYLLPRGPRGLGVRATKTSERSQPRG 60
DB 1 MSTNPKQKKNKNTNRPPQDVKPPGGQIVGGVYLLPRGPRGLGVRATKTSERSQPRG 60

QY 61 RROPIKARPEGRGRTWAQPGYWPPLYGNEGCGWAGWLLSPRGSR-PSWGPTDPRRSRNL 119
DB 61 RROPIKARPEGRGRTWAQPGYWPPLYGNEGCGWAGWLLSPRGSRGSWG-TDPRRSRNL 119

QY 120 GKVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLL 179
DB 120 GKVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLL 179

QY 180 ALLSCLTVPASA 191
DB 180 ALLSCLTVPASA 191

RESULT 15
A45573
genome polyprotein - hepatitis C virus (strain JT)
N;Contains: capsid protein C; envelope protein M; hepatitis C virus (strain JT) (nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: A45573
R;Tanaka, T.; Kato, N.; Nakagawa, M.; Ootsuyama, Y.; Cho, M.J.; Nakazawa, T.; Hijikata, Y. Virus Res. 23, 39-53, 1992
A>Title: Molecular cloning of hepatitis C virus genome from a single Japanese carrier: B
A;Reference number: A45573; MUID:92295714; PMID:1318627
A;Accession: A45573
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3010 <TAN>
A;Cross-references: UNIPROT:Q00269; GB:D11168; GB:D01171; NID:G221612; PIDN:BAA01943.1; A;Experimental source: HCV-JT
A;Note: Sequence extracted from NCBI backbone (NCBI:106206, NCBI:106207)
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serine
F;2-115/Product: capsid protein C #status predicted <CPC>
F;116-191/Product: envelope protein M #status predicted <EPM>
F;192-389/Product: major envelope protein E #status predicted <MEE>
F;390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F;730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F;1007-1615/Product: hepatitis C virus genome polyprotein
F;1230-1237/Region: nucleotide-binding motif A (P-loop)
F;1312-1317/Region: nucleotide-binding motif B
F;1316-1319/Region: DEXH motif
F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4a>
F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4b>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>

Query Match 96.0%; Score 998; DB 1; Length 3010;
Best Local Similarity 95.8%; Pred. No. 2.6e-74;
Matches 183; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNKNTNRPPQDVKPPGGQIVGGVYLLPRGPRGLGVRATKTSERSQPRG 60
DB 1 MSTNPKQKKNKNTNRPPQDVKPPGGQIVGGVYLLPRGPRGLGVRATKTSERSQPRG 60

Search completed: August 19, 2005, 12:44:07
Job time : 25 secs

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DB 61 RROPIKARPEGRGRTWAQPGYWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRSRNLG 120

QY 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180

QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 19, 2005, 12:43:21 ; Search time 107 Seconds
(without alignments)
698.999 Million cell updates/sec

Title: US-10-770-117-4

Perfect score: 1040

Sequence: 1 MSTNPKQKKNKNTNRPPQ.....CSPSIFLLALLSCLTVPASA 191

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1040	100.0	191	18	US-10-770-117-4
2	1040	100.0	3011	9	US-09-916-359-2
3	1040	100.0	3011	16	US-10-445-724-2
4	1036	99.6	190	14	US-10-268-562-1
5	1035	99.5	190	15	US-10-450-649-7
6	1035	99.5	191	18	US-10-770-117-2
7	1031	99.1	249	15	US-10-365-620-54
8	1031	99.1	249	17	US-10-912-969-56
9	1031	99.1	450	15	US-10-912-969-56
10	1031	99.1	450	15	US-10-651-165-179
11	1031	99.1	473	15	US-10-651-165-180
					US-10-365-620-56
					Sequence 4, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 1, Appli
					Sequence 7, Appli
					Sequence 2, Appli
					Sequence 54, Appli
					Sequence 56, Appli
					Sequence 179, App
					Sequence 180, App
					Sequence 56, Appl

12	1031	99.1	473	17	US-10-912-969-58
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14	1031	99.1	3011	9	US-09-742-659-4
15	1031	99.1	3011	9	US-09-952-572-9
16	1031	99.1	3011	9	US-09-929-955-1
17	1031	99.1	3011	9	US-09-747-419-20
18	1031	99.1	3011	9	US-09-891-894-3
19	1031	99.1	3011	13	US-10-104-966-1
20	1031	99.1	3011	14	US-10-259-275-20
21	1031	99.1	3011	14	US-10-184-150-3
22	1031	99.1	3011	15	US-10-328-997-3
23	1031	99.1	3011	15	US-10-189-359-14
24	1031	99.1	3011	15	US-10-296-734-406
25	1031	99.1	3011	15	US-10-719-619-1
26	1031	99.1	3011	16	US-10-817-591-1
27	1031	99.1	3011	20	US-11-006-313-20
28	1031	99.1	3012	9	US-09-238-076-2
29	1031	99.1	3012	10	US-09-995-937-2
30	1031	99.1	3012	10	US-09-917-563-2
31	1027	98.8	3011	9	US-09-238-076-20
32	1027	98.8	3011	10	US-09-995-937-20
33	1027	98.8	3011	10	US-09-917-563-20
34	1020	98.1	450	15	US-10-651-165-187
35	1018	97.9	450	15	US-10-651-165-181
36	1018	97.9	2894	9	US-09-941-611-23
37	1018	97.9	2894	14	US-10-044-995-23
38	1018	97.9	2894	17	US-10-822-871-23
39	1016	97.7	450	15	US-10-651-165-190
40	1016	97.7	3011	14	US-10-232-643-6
41	1012	97.3	809	9	US-09-973-025-50
42	1012	97.3	809	10	US-09-899-303-50
43	1012	97.3	809	10	US-09-995-808-50
44	1012	97.3	809	10	US-09-995-860-50
45	1012	97.3	809	10	US-09-995-791-50

ALIGNMENTS

RESULT 1

US-10-770-117-4
; Sequence 4, Application US/10770117
; Publication No. US20050129705A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States, as represented by the
; APPLICANT: Secretary, Dept. of
; APPLICANT: Health and Human Services
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Sarobe, Pablo
; APPLICANT: Pendleton, C. David
; APPLICANT: Feinstein, Stephen M.
; APPLICANT: Arichi, Tatsumi
; APPLICANT: Major, Marian E.
; TITLE OF INVENTION: MODIFIED HCV PEPTIDE VACCINES
; FILE REFERENCE: 14014.0347/P
; CURRENT APPLICATION NUMBER: US/10/770,117
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: US/09/763,260
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/097,446
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: synthetic construct
US-10-770-117-4

Query Match 100.0%; Score 1040; DB 18; Length 191;

Best Local Similarity 100.0%; Pred. No. 5.7e-81;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKKNTNRRPQDVKFGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKQKKKNTNRRPQDVKFGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60

Qy 61 RRQIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120
Db 61 RRQIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120

Qy 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 2

US-09-916-359-2
; Sequence 2, Application US/09916359
; Patent No. US20020034734A1
; GENERAL INFORMATION:
; APPLICANT: Veronique Barban
; TITLE OF INVENTION: VACCINE COMPOSITION FOR PREVENTING OR
; TITLE OF INVENTION: TREATING C HEPATITIS
; FILE REFERENCE: PMCF97-03A
; CURRENT APPLICATION NUMBER: US/09/916.359
; CURRENT FILING DATE: 2001-07-26
; PRIOR FILING DATE: 1999-09-02
; PRIOR FILING DATE: 1997-03-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3011
; TYPE: PRT
; ORGANISM: Virus
US-09-916-359-2

Query Match 100.0%; Score 1040; DB 9; Length 3011;
Best Local Similarity 100.0%; Pred. No. 1.1e-79;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSTNPKQKKKNTNRRPQDVKFGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60

Qy 61 RRQIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120
Db 61 RRQIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120

Qy 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 3

US-10-445-724-2
; Sequence 2, Application US/10445724
; Publication No. US20040101829A1
; GENERAL INFORMATION:
; APPLICANT: STAPLETON, JACK T.
; APPLICANT: WUENSCHMANN, SABINA
; TITLE OF INVENTION: A PROTEIN THAT INTERACTS WITH LIPIDS AND
; TITLE OF INVENTION: METHODS FOR TREATING HYPERLIPIDEMIA

; FILE REFERENCE: IOWA:045US
; CURRENT APPLICATION NUMBER: US/10/445,724
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: 60/392,158
; PRIOR FILING DATE: 2003-05-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3011
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-445-724-2

Query Match 100.0%; Score 1040; DB 16; Length 3011;
Best Local Similarity 100.0%; Pred. No. 1.1e-79;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKKNTNRRPQDVKFGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKQKKKNTNRRPQDVKFGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60

Qy 61 RRQIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120
Db 61 RRQIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120

Qy 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 4

US-10-268-562-1
; Sequence 1, Application US/10268562
; Publication No. US20030108563A1
; GENERAL INFORMATION:
; APPLICANT: Ocho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: Reagents for the simultaneous detection of HCV core antigens and
; TITLE OF INVENTION: antibodies
; FILE REFERENCE: CDS0287
; CURRENT APPLICATION NUMBER: US/10/268,562
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/347,943
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-268-562-1

Query Match 99.6%; Score 1036; DB 14; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.2e-80;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKKNTNRRPQDVKFGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKQKKKNTNRRPQDVKFGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60

Qy 61 RRQIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120
Db 61 RRQIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120

Qy 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 190
Db 181 LLSCLTVPASA 190

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Db      181 LLSCLTVPAS 190

RESULT 5
US-10-450-649-7
; Sequence 7, Application US/10450649
; Publication No. US20040052818A1
; GENERAL INFORMATION:
; APPLICANT: Heinz, Franz X.
; APPLICANT: Mandl, Christian
; TITLE OF INVENTION: ATTENUATED LIVE VACCINE
; FILE REFERENCE: U 014666-0
; CURRENT APPLICATION NUMBER: US/10/450,649
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/AT02/00046
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: A 272/2001 AT
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Hepatitis C Virus 1
US-10-450-649-7

Query Match      99.5%; Score 1035; DB 15; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.5e-80;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 STNPKPKKKNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVTRATKTSERSQPRGR 61
Db      1 STNPKPKKKNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVTRATKTSERSQPRGR 60

Qy      62 RQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLGK 121
Db      61 RQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLGK 120

Qy      122 VIDTLTCGFADLMGYIPLVGAPLGGARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 181
Db      121 VIDTLTCGFADLMGYIPLVGAPLGGARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180

Qy      182 LLSCLTVPASA 191
Db      181 LLSCLTVPASA 190

RESULT 6
US-10-770-117-2
; Sequence 2, Application US/10770117
; Publication No. US20050129705A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States, as represented by the
; APPLICANT: Secretary, Dept. of
; APPLICANT: Health and Human Services
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Sarobe, Pablo
; APPLICANT: Pendleton, C. David
; APPLICANT: Feinstein, Stephen M.
; APPLICANT: Arichi, Tatsumi
; APPLICANT: Major, Marian E.
; TITLE OF INVENTION: MODIFIED HCV PEPTIDE VACCINES
; FILE REFERENCE: 14014.0347/P
; CURRENT APPLICATION NUMBER: US/10/770,117
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: US/09/763,260
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/097,446
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 191

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: synthetic construct
US-10-770-117-2

Query Match      99.5%; Score 1035; DB 18; Length 191;
Best Local Similarity 99.5%; Pred. No. 1.5e-80;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MSTNPKPKKKNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVTRATKTSERSQPRG 60
Db      1 MSTNPKPKKKNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVTRATKTSERSQPRG 60

Qy      61 RQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120
Db      61 RQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120

Qy      121 KVIDTLTCGFADLMGYIPLVGAPLGGARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db      121 KVIDTLTCGFADLMGYIPLVGAPLGGARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180

Qy      181 LLSCLTVPASA 191
Db      181 LLSCLTVPASA 191

RESULT 7
US-10-365-620-54
; Sequence 54, Application US/10365620
; Publication No. US20040001853A1
; GENERAL INFORMATION:
; APPLICANT: George, Rajan
; APPLICANT: Tyrrell, Lorne
; TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response
; FILE REFERENCE: 656.0016
; CURRENT APPLICATION NUMBER: US/10/365,620
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US60/423,578
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: 60/390,564
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 249
; TYPE: PRT
; ORGANISM: ORF of HCV Core Protein
US-10-365-620-54

Query Match      99.1%; Score 1031; DB 15; Length 249;
Best Local Similarity 99.0%; Pred. No. 4.4e-80;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MSTNPKPKKKNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVTRATKTSERSQPRG 60
Db      31 MSTNPKPKKKNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVTRATKTSERSQPRG 90

Qy      61 RQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120
Db      91 RQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 150

Qy      121 KVIDTLTCGFADLMGYIPLVGAPLGGARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db      151 KVIDTLTCGFADLMGYIPLVGAPLGGARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 210

Qy      181 LLSCLTVPASA 191
Db      211 LLSCLTVPASA 221
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```
RESULT 8
US-10-912-969-56
; Sequence 56, Application US/10912969
; Publication No. US20050013828A1
; GENERAL INFORMATION:
; APPLICANT: Virex Research, Inc.
; APPLICANT: George, Rajan
; APPLICANT: Tyrrell, Lorne
; APPLICANT: Noujaim, Antoine
; APPLICANT: Wang, Dakun
; APPLICANT: Ma, Allan
; TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response
; FILE REFERENCE: 17506-007001
; CURRENT APPLICATION NUMBER: US/10/912,969
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: US 60/390,564
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 60/423,578
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 10/365,620
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: PCT/IB04/00373
; PRIOR FILING DATE: 2004-02-14
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-912-969-56

Query Match          99.1%; Score 1031; DB 17; Length 249;
Best Local Similarity 99.0%; Pred. No. 4.4e-80;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNTNRRPQDVKFGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60
   |||||:|||||
Db 31 MSTNPKQRTKNTNRRPQDVKFGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 90
   |||||:|||||

QY 61 RRQPIKARRPEGRRTWAQGYWPPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120
   |||||:|||||
Db 91 RRQPIKARRPEGRRTWAQGYWPPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 150
   |||||:|||||

QY 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
   |||||:|||||
Db 151 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 210
   |||||:|||||

QY 181 LLSCLTVPASA 191
   |||||:|||||
Db 211 LLSCLTVPASA 221
   |||||:|||||

RESULT 9
US-10-651-165-179
; Sequence 179, Application US/10651165
; Publication No. US20040047877A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 179
; LENGTH: 450
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-179

Query Match          99.1%; Score 1031; DB 15; Length 450;
Best Local Similarity 99.0%; Pred. No. 8.3e-80;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNTNRRPQDVKFGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60
   |||||:|||||
Db 1 MSTNPKQRTKNTNRRPQDVKFGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60
   |||||:|||||

QY 61 RRQPIKARRPEGRRTWAQGYWPPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120
   |||||:|||||
Db 61 RRQPIKARRPEGRRTWAQGYWPPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120
   |||||:|||||

QY 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
   |||||:|||||
Db 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
   |||||:|||||

QY 181 LLSCLTVPASA 191
   |||||:|||||
Db 181 LLSCLTVPASA 191
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RESULT 11
US-10-365-620-56
; Sequence 56, Application US/10365620
; Publication No. US20040001853A1
; GENERAL INFORMATION:
; APPLICANT: George, Rajan
; APPLICANT: Tyrell, Lorne
; APPLICANT: No. US20040001853A1ajam, Antoine
; TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response
; FILE REFERENCE: 656.0016
; CURRENT APPLICATION NUMBER: US/10/365,620
; CURRENT FILING DATE: 2003-02-13
; PRIOR FILING DATE: 2003-11-05
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 473
; TYPE: PRT
; ORGANISM: ORF of HCV Core-TBD protein
US-10-365-620-56

Query Match          99.1%; Score 1031; DB 15; Length 473;
Best Local Similarity 99.0%; Pred. No. 8.8e-80;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKPKQKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 60
DB 31 MSTNPKPQRTKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 90
QY 61 RRQPIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120
DB 91 RRQPIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 150
QY 121 KVDTLTTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
DB 151 KVDTLTTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 210
QY 181 LLSCLTVPASA 191
DB 211 LLSCLTVPASA 221

RESULT 12
US-10-912-969-58
; Sequence 58, Application US/10912969
; Publication No. US20050013828A1
; GENERAL INFORMATION:
; APPLICANT: Virexx Research, Inc.
; APPLICANT: George, Rajan
; APPLICANT: Tyrell, Lorne
; APPLICANT: Noujaim, Antoine
; APPLICANT: Wang, Dakun
; APPLICANT: Ma, Allan
; TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response
; FILE REFERENCE: 17506-007001
; CURRENT APPLICATION NUMBER: US/10/912,969
; CURRENT FILING DATE: 2004-08-05
; PRIOR FILING DATE: 2002-06-20
; PRIOR FILING DATE: 2002-11-05
; PRIOR FILING DATE: 2003-02-13
; PRIOR FILING DATE: 2004-02-14
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
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; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-912-969-58

Query Match          99.1%; Score 1031; DB 17; Length 473;
Best Local Similarity 99.0%; Pred. No. 8.8e-80;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKPKQKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 60
DB 31 MSTNPKPQRTKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 90
QY 61 RRQPIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120
DB 91 RRQPIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 150
QY 121 KVDTLTTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
DB 151 KVDTLTTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 210
QY 181 LLSCLTVPASA 191
DB 211 LLSCLTVPASA 221

RESULT 13
US-10-913-171-39
; Sequence 39, Application US/10913171
; Publication No. US20050031628A1
; GENERAL INFORMATION:
; APPLICANT: Virexx Research, Inc.
; APPLICANT: George, Rajan
; APPLICANT: Tyrell, Lorne
; APPLICANT: Noujaim, Antoine
; APPLICANT: Wang, Dakun
; APPLICANT: Ma, Allan
; TITLE OF INVENTION: CHIMERIC ANTIGENS FOR BREAKING HOST TOLERANCE TO FOREIGN ANTIGENS
; FILE REFERENCE: 17506-006001
; CURRENT APPLICATION NUMBER: US/10/913,171
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: US 60/493,449
; PRIOR FILING DATE: 2004-08-08
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-913-171-39

Query Match          99.1%; Score 1031; DB 17; Length 473;
Best Local Similarity 99.0%; Pred. No. 8.8e-80;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKPKQKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 60
DB 31 MSTNPKPQRTKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 90
QY 61 RRQPIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120
DB 91 RRQPIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 150
QY 121 KVDTLTTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
DB 151 KVDTLTTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 210
QY 181 LLSCLTVPASA 191
DB 211 LLSCLTVPASA 221
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OM protein - protein search, using sw model

Run on: August 19, 2005, 12:34:55 ; Search time 20 Seconds
(without alignments)
712.899 Million cell updates/sec

Title: US-10-770-117-4

Perfect score: 1040

Sequence: 1 MSTNPKQKKNKNTNRPO.....CSPSIFLLALLSCLTVPASA 191

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1040	100.0	191	4	US-09-763-260-4
2	1040	100.0	3011	1	US-08-440-103-36
3	1040	100.0	3011	1	US-08-440-542-36
4	1040	100.0	3011	1	US-07-910-760-10
5	1040	100.0	3011	1	US-08-440-519-10
6	1040	100.0	3011	1	US-08-231-368-36
7	1040	100.0	3011	1	US-08-440-210-36
8	1040	100.0	3011	3	US-09-388-874-2
9	1040	100.0	3011	3	US-09-046-604-36
10	1040	100.0	3011	3	US-08-440-549-10
11	1040	100.0	3011	3	US-08-850-328-1
12	1040	100.0	3011	4	US-09-916-359-2
13	1036	99.6	215	1	US-07-681-703B-12
14	1036	99.6	215	1	US-07-681-703B-14
15	1036	99.6	215	5	PCT-US91-02370-12
16	1036	99.6	215	5	PCT-US91-02370-14
17	1036	99.6	217	2	US-08-407-410B-12
18	1036	99.6	217	2	US-08-407-410B-14
19	1036	99.6	217	2	US-08-485-500-12
20	1036	99.6	217	2	US-08-485-500-14
21	1035	99.5	191	4	US-09-763-260-2
22	1034	99.4	2995	3	US-08-444-818-138
23	1031	99.1	191	2	US-08-290-665A-156
24	1031	99.1	191	2	US-08-290-665A-157
25	1031	99.1	191	2	US-08-290-665A-158
26	1031	99.1	191	2	US-08-290-665A-159
27	1031	99.1	191	2	US-08-290-665A-160

28	1031	99.1	191	3	US-08-380-160-3	Sequence 3, Appli
29	1031	99.1	191	5	PCT-US95-10398-156	Sequence 156, App
30	1031	99.1	191	5	PCT-US95-10398-157	Sequence 157, App
31	1031	99.1	191	5	PCT-US95-10398-158	Sequence 158, App
32	1031	99.1	191	5	PCT-US95-10398-159	Sequence 159, App
33	1031	99.1	191	5	PCT-US95-10398-160	Sequence 160, App
34	1031	99.1	191	5	PCT-US95-10398-161	Sequence 179, App
35	1031	99.1	450	4	US-08-635-886C-179	Sequence 180, App
36	1031	99.1	450	4	US-08-635-886C-180	Sequence 179, App
37	1031	99.1	450	4	US-08-974-690C-179	Sequence 180, App
38	1031	99.1	450	4	US-08-974-690C-180	Sequence 13, Appli
39	1031	99.1	967	5	PCT-US94-07280-13	Sequence 13, Appli
40	1031	99.1	967	5	PCT-US95-01087-13	Sequence 13, Appli
41	1031	99.1	1648	1	US-08-188-281B-12	Sequence 12, Appli
42	1031	99.1	1648	5	PCT-US94-07280-12	Sequence 12, Appli
43	1031	99.1	1648	5	PCT-US95-01087-12	Sequence 12, Appli
44	1031	99.1	3011	1	US-08-188-281B-1	Sequence 1, Appli
45	1031	99.1	3011	1	US-08-453-552-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-763-260-4
; Sequence 4, Application US/09763260
; Patent No. 6685944
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States, as represented by the
; APPLICANT: Secretary, Dept. of
; APPLICANT: Health and Human Services
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Sarobe, Pablo
; APPLICANT: Pendleton, C. David
; APPLICANT: Feinstein, Stephen M.
; APPLICANT: Arichi, Tatsumi
; APPLICANT: Major, Marian E.
; TITLE OF INVENTION: MODIFIED HCV PEPTIDE VACCINES
; FILE REFERENCE: 14014.0347/P
; CURRENT APPLICATION NUMBER: US/09/763,260
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/097,446
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. 6685944e =
; OTHER INFORMATION: synthetic construct
US-09-763-260-4

Query Match	100.0%;	Score	1040;	DB	4;	Length	191;
Best Local Similarity	100.0%;	Pred. No.	4.5e-94;				
Matches	191;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	1	MSTNPKQKKNKNTNRPODVKFGGQIVGGVYLLPRGPRILGVATRTKTSERSOPRG	60				
Qy	61	RRQIPKARPEGRWAQPGYPWPLYGNECGWAGWLLSPRGSRPSPWGPTDPRRRSNL	120				
Db	61	RRQIPKARPEGRWAQPGYPWPLYGNECGWAGWLLSPRGSRPSPWGPTDPRRRSNL	120				
Qy	121	KVIDTLTCGFADLMGYIPLVGAFLGGAARALAHGVRVLEQGVNYATGNLPCGSFIS	180				
Db	121	KVIDTLTCGFADLMGYIPLVGAFLGGAARALAHGVRVLEQGVNYATGNLPCGSFIS	180				
Qy	181	LLSCLTVPASA	191				
Db	181	LLSCLTVPASA	191				

RESULT 2
US-08-440-103-36
; Sequence 36, Application US/08440103
; Patent No. 5670152
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,103
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3011 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-440-103-36

Query Match 100.0%; Score 1040; DB 1; Length 3011;
Best Local Similarity 100.0%; Pred. No. 1.3e-92;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
QY 61 RRQPIKARRPEGRTPWAQGYPMPLVYNECGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
Db 61 RRQPIKARRPEGRTPWAQGYPMPLVYNECGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
QY 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 3
US-08-440-542-36
; Sequence 36, Application US/08440542
; Patent No. 5670153

; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,542
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3011 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-440-542-36

Query Match 100.0%; Score 1040; DB 1; Length 3011;
Best Local Similarity 100.0%; Pred. No. 1.3e-92;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
QY 61 RRQPIKARRPEGRTPWAQGYPMPLVYNECGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
Db 61 RRQPIKARRPEGRTPWAQGYPMPLVYNECGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
QY 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 4
US-07-910-760-10
; Sequence 10, Application US/07910760
; Patent No. 5683864
; GENERAL INFORMATION:
; APPLICANT: Houghton, Michael
; APPLICANT: Choo, Qui-Liam
; APPLICANT: Kuo, George
; TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV)
; TITLE OF INVENTION: Antigens for Use in Immunoassays for Anti-HCV Antibodies

```
;
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: P.O. Box 8097 (Int. Prop. R-440)
; CITY: Emeryville
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/910,760
; FILING DATE: 07-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Blackburn Esq., Robert P.
; REGISTRATION NUMBER: 30,447
; REFERENCE/DOCKET NUMBER: 0101.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2702
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3011 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-910-760-10

Query Match 100.0%; Score 1040; DB 1; Length 3011;
Best Local Similarity 100.0%; Pred. No. 1.3e-92;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTNPKPKQKNKNTNRRPQDVKPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKPKQKNKNTNRRPQDVKPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60

Qy 61 RRQIPKARRPEGRWTAQPGYPWLYGNEGCGWAGWLLSPRGRSPSGMPTDPRRRSRNLG 120
Db 61 RRQIPKARRPEGRWTAQPGYPWLYGNEGCGWAGWLLSPRGRSPSGMPTDPRRRSRNLG 120

Qy 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 5
US-08-440-519-10
; Sequence 10, Application US/08440519
; Patent No. 5712087
; GENERAL INFORMATION:
; APPLICANT: Houghton, Michael
; APPLICANT: Choo, Qui-Lim
; APPLICANT: Kuo, George
; TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV)
; TITLE OF INVENTION: Antigens for Use in Immunoassays for Anti-HCV Antibodies
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: P.O. Box 8097 (Int. Prop. R-440)
; CITY: Emeryville
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,519
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/910,760
; FILING DATE: 07-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Blackburn Esq., Robert P.
; REGISTRATION NUMBER: 30,447
; REFERENCE/DOCKET NUMBER: 0101.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2702
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3011 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-440-519-10

Query Match 100.0%; Score 1040; DB 1; Length 3011;
Best Local Similarity 100.0%; Pred. No. 1.3e-92;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTNPKPKQKNKNTNRRPQDVKPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKPKQKNKNTNRRPQDVKPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60

Qy 61 RRQIPKARRPEGRWTAQPGYPWLYGNEGCGWAGWLLSPRGRSPSGMPTDPRRRSRNLG 120
Db 61 RRQIPKARRPEGRWTAQPGYPWLYGNEGCGWAGWLLSPRGRSPSGMPTDPRRRSRNLG 120

Qy 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 6
US-08-231-368-36
; Sequence 36, Application US/08231368
; Patent No. 5756312
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,575
```

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; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3011 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-440-210-36

Query Match 100.0%; Score 1040; DB 1; Length 3011;
Best Local Similarity 100.0%; Pred. No. 1.3e-92;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTNPKPKQKKKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
DB 1 MSTNPKPKQKKKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
QY 61 RRQPIPKARRPEGRRTWAQPGYWPPLYGNECCGAGWLLSPRGSRSWGPDPRRSRNLG 120
DB 61 RRQPIPKARRPEGRRTWAQPGYWPPLYGNECCGAGWLLSPRGSRSWGPDPRRSRNLG 120
QY 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRLVEDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRLVEDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191

RESULT 7
US-08-440-210-36
; Sequence 36, Application US/08440210
; Patent No. 5766845
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,210
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:

; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3011 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-440-210-36

Query Match 100.0%; Score 1040; DB 1; Length 3011;
Best Local Similarity 100.0%; Pred. No. 1.3e-92;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTNPKPKQKKKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
DB 1 MSTNPKPKQKKKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
QY 61 RRQPIPKARRPEGRRTWAQPGYWPPLYGNECCGAGWLLSPRGSRSWGPDPRRSRNLG 120
DB 61 RRQPIPKARRPEGRRTWAQPGYWPPLYGNECCGAGWLLSPRGSRSWGPDPRRSRNLG 120
QY 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRLVEDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRLVEDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191

RESULT 8
US-09-388-874-2
; Sequence 2, Application US/09388874
; Patent No. 6284249
; GENERAL INFORMATION:
; APPLICANT: Veronique Barban
; TITLE OF INVENTION: VACCINE COMPOSITION FOR PREVENTING OR
; FILE REFERENCE: PMCF97-03A
; CURRENT APPLICATION NUMBER: US/09/388,874
; CURRENT FILING DATE: 1999-09-02
; EARLIER APPLICATION NUMBER: PCT/FR98/00448
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 97/02,887
; EARLIER FILING DATE: 1997-03-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3011
; TYPE: PRT
; ORGANISM: Virus
; US-09-388-874-2

Query Match 100.0%; Score 1040; DB 3; Length 3011;
Best Local Similarity 100.0%; Pred. No. 1.3e-92;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTNPKPKQKKKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
DB 1 MSTNPKPKQKKKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
QY 61 RRQPIPKARRPEGRRTWAQPGYWPPLYGNECCGAGWLLSPRGSRSWGPDPRRSRNLG 120
DB 61 RRQPIPKARRPEGRRTWAQPGYWPPLYGNECCGAGWLLSPRGSRSWGPDPRRSRNLG 120
QY 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRLVEDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRLVEDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191
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Db      181  LLSCLTVPASA 191

RESULT 9
US-09-046-604-36
; Sequence 36, Application US/0904604
; Patent No. 6303292
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,604
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3011 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-046-604-36

Query Match      100.0%; Score 1040; DB 3; Length 3011;
Best Local Similarity 100.0%; Pred. No. 1.3e-92;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MSTNPKQKKNTNRRPQDVKPGGQIVGGVYLLPRRGPRLGVTRATKTSERSQPRG 60
Db      1  MSTNPKQKKNTNRRPQDVKPGGQIVGGVYLLPRRGPRLGVTRATKTSERSQPRG 60

Qy      61  RRQPIPKARPEGRTPAQPGYPWPLYNCGCGWAGLLSPRGSRPSPWGPTDPRRRSRNLG 120
Db      61  RRQPIPKARPEGRTPAQPGYPWPLYNCGCGWAGLLSPRGSRPSPWGPTDPRRRSRNLG 120

Qy      121  KVDTLTTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEGVNYATGNLPGCSFSIFLLA 180
Db      121  KVDTLTTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEGVNYATGNLPGCSFSIFLLA 180

Qy      181  LLSCLTVPASA 191
Db      181  LLSCLTVPASA 191

RESULT 10
US-08-440-549-10
; Sequence 10, Application US/08440549
; Patent No. 6379886
; GENERAL INFORMATION:
; APPLICANT: TAKAHAMA, Y.
; APPLICANT: SHIRAIISHI, J.
; TITLE OF INVENTION: DIAGNOSTIC REAGENT FOR HEPATITIS
; TITLE OF INVENTION: C VIRUS INFECTION
; NUMBER OF SEQUENCES: 13
; Patent No. 6312889
; GENERAL INFORMATION:
; APPLICANT: Houghton, Michael
; APPLICANT: Choo, Qui-Lim
; APPLICANT: Kuo, George
; TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV)
; TITLE OF INVENTION: Antigens for Use in Immunoassays for Anti-HCV Antibodies
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: P.O. Box 8097 (Int. Prop. R-440)
; CITY: Emeryville
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,549
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/910,760
; FILING DATE: 07-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Blackburn Esq., Robert P.
; REGISTRATION NUMBER: 30,447
; REFERENCE/DOCKET NUMBER: 0101.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2702
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3011 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-440-549-10

Query Match      100.0%; Score 1040; DB 3; Length 3011;
Best Local Similarity 100.0%; Pred. No. 1.3e-92;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MSTNPKQKKNTNRRPQDVKPGGQIVGGVYLLPRRGPRLGVTRATKTSERSQPRG 60
Db      1  MSTNPKQKKNTNRRPQDVKPGGQIVGGVYLLPRRGPRLGVTRATKTSERSQPRG 60

Qy      61  RRQPIPKARPEGRTPAQPGYPWPLYNCGCGWAGLLSPRGSRPSPWGPTDPRRRSRNLG 120
Db      61  RRQPIPKARPEGRTPAQPGYPWPLYNCGCGWAGLLSPRGSRPSPWGPTDPRRRSRNLG 120

Qy      121  KVDTLTTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEGVNYATGNLPGCSFSIFLLA 180
Db      121  KVDTLTTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEGVNYATGNLPGCSFSIFLLA 180

Qy      181  LLSCLTVPASA 191
Db      181  LLSCLTVPASA 191

RESULT 11
US-08-850-328-1
; Sequence 1, Application US/08850328
; Patent No. 6379886
; GENERAL INFORMATION:
; APPLICANT: TAKAHAMA, Y.
; APPLICANT: SHIRAIISHI, J.
; TITLE OF INVENTION: DIAGNOSTIC REAGENT FOR HEPATITIS
; TITLE OF INVENTION: C VIRUS INFECTION
; NUMBER OF SEQUENCES: 13
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,328
; FILING DATE: 02-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mays, Thomas D
; REGISTRATION NUMBER: 34,524
; REFERENCE/DOCKET NUMBER: 32273-20004.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3011 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-850-328-1

Query Match 100.0%; Score 1040; DB 3; Length 3011;
Best Local Similarity 100.0%; Pred. No. 1.3e-92;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTNPKPKQKNKNTNRRPDQVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
Db 1 MSTNPKPKQKNKNTNRRPDQVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
Qy 61 RRQPIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRSRNLG 120
Db 61 RRQPIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRSRNLG 120
Qy 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 13
US-07-681-703B-12
; Sequence 12, Application US/07681703B
; Patent No. 5443965
; GENERAL INFORMATION:
; APPLICANT: Reyes, Gregory
; APPLICANT: Kim, Jungsu P.
; APPLICANT: Moeckli, Randolph
; TITLE OF INVENTION: Hepatitis C Virus Epitopes
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/681,703B
; FILING DATE: 05-APR-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 505,611
; FILING DATE: 06-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 594,854
; FILING DATE: 09-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-076.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-681-703B-12

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/916,359
; FILING DATE: 2001-07-26
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/388,874
; FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 97/02,887
; PRIOR FILING DATE: 1997-03-06
; NUMBER OF SEQ ID NOS: 2

Query Match 100.0%; Score 1040; DB 3; Length 3011;
Best Local Similarity 100.0%; Pred. No. 1.3e-92;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTNPKPKQKNKNTNRRPDQVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
Db 1 MSTNPKPKQKNKNTNRRPDQVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
Qy 61 RRQPIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRSRNLG 120
Db 61 RRQPIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGRSPSWGPTDPRRSRNLG 120
Qy 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 12
US-09-916-359-2
; Sequence 2, Application US/09916359
; Patent No. 6538123
; GENERAL INFORMATION:
; APPLICANT: Veronique Barban
; TITLE OF INVENTION: VACCINE COMPOSITION FOR PREVENTING OR
; FILE REFERENCE: PMCF97-03A
; CURRENT APPLICATION NUMBER: US/09/916,359
; FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 09/388,874
; FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 97/02,887
; FILING DATE: 1997-03-06
; NUMBER OF SEQ ID NOS: 2
```

Query Match 99.6%; Score 1036; DB 1; Length 215;
Best Local Similarity 99.5%; Pred. No. 1.3e-93;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNTNRRPDVKFPGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60
Db 1 MGTNPKQKKNTNRRPDVKFPGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

Qy 61 RRQPIPKARRPEGRWTAQPGYPMPLVGNCGWAGWLLSPRGRPSWGPTDPRRSNGLG 120
Db 61 RRQPIPKARRPEGRWTAQPGYPMPLVGNCGWAGWLLSPRGRPSWGPTDPRRSNGLG 120

Qy 121 KVIDTLTCGFADLMGYIPLVGAAPLGGAARALAHGVRLVDGVNATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPLVGAAPLGGAARALAHGVRLVDGVNATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 14

US-07-681-703B-14
; Sequence 14, Application US/07681703B
; Patent No. 5443965
; GENERAL INFORMATION:
; APPLICANT: Reyes, Gregory
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Moeckli, Randolph
; TITLE OF INVENTION: Hepatitis C Virus Epitopes
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/681.703B
; FILING DATE: 05-APR-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 505,611
; FILING DATE: 06-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 594,854
; FILING DATE: 09-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-076.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-681-703B-14

Query Match 99.6%; Score 1036; DB 1; Length 215;
Best Local Similarity 99.5%; Pred. No. 1.3e-93;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNTNRRPDVKFPGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

Db 1 MGTNPKQKKNTNRRPDVKFPGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

Qy 61 RRQPIPKARRPEGRWTAQPGYPMPLVGNCGWAGWLLSPRGRPSWGPTDPRRSNGLG 120

Db 61 RRQPIPKARRPEGRWTAQPGYPMPLVGNCGWAGWLLSPRGRPSWGPTDPRRSNGLG 120

Qy 121 KVIDTLTCGFADLMGYIPLVGAAPLGGAARALAHGVRLVDGVNATGNLPGCSFSIFLLA 180

Db 121 KVIDTLTCGFADLMGYIPLVGAAPLGGAARALAHGVRLVDGVNATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 15
PCT-US91-02370-12
; Sequence 12, Application PC/TUS9102370
; GENERAL INFORMATION:
; APPLICANT: Reyes, Gregory
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Moeckli, Randolph
; APPLICANT: Simonsen, Christian C.
; TITLE OF INVENTION: Hepatitis C Virus Epitopes
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Peter J. Dehlinger
; STREET: P.O. BOX 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02370
; FILING DATE: 19910405
; CLASSIFICATION: 435.5
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 505,611
; FILING DATE: 06-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 594,854
; FILING DATE: 09-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-076.41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 323-8302
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US91-02370-12

Query Match 99.6%; Score 1036; DB 5; Length 215;
Best Local Similarity 99.5%; Pred. No. 1.3e-93;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNTNRRPDVKFPGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

Db 1 MGTNPKQKKNTNRRPDVKFPGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

Qy 61 RRQPIPKARRPEGRWTAQPGYPMPLVGNCGWAGWLLSPRGRPSWGPTDPRRSNGLG 120

Db 61 RRQPIPKARRPEGRWTAQPGYPMPLVGNCGWAGWLLSPRGRPSWGPTDPRRSNGLG 120

Qy	121	KVIDTLTCGFADLMGYIPLV	GADPLGGAARALAHGVRVLE	DGVNYATGNLPGCSFSIFLLA	180
Db	121	KVIDTLTCGFADLMGYIPLV	GADPLGGAARALAHGVRVLE	DGVNYATGNLPGCSFSIFLLA	180
Qy	181	LLSCLTVPASA	191		
Db	181	LLSCLTVPASA	191		

Search completed: August 19, 2005, 12:44:53
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 19, 2005, 12:28:45 ; Search time 117.5 Seconds
(without alignments)
628.691 Million cell updates/sec

Title: US-10-770-117-4

Perfect score: 1040

Sequence: 1 MSTNPKPQKGNKNTNRPO.....CSFSIFLLALLSLCTVPASA 191

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1980s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1040	100.0	191	3	AAY82999 Hepatitis
2	1040	100.0	2816	2	AAR34009 HCV-1 pol
3	1040	100.0	2955	2	AAY14975 Amino aci
4	1040	100.0	2955	3	AAB18541 Polypeptide
5	1040	100.0	3011	2	AAR21519 Compiled
6	1040	100.0	3011	2	AAR90931 Hepatitis
7	1040	100.0	3011	2	AAR34480 HCV poly
8	1040	100.0	3011	2	AAR40038 HCV poly
9	1040	100.0	3011	5	AAR22049 Hepatitis
10	1040	100.0	3011	8	ADL23107 Hepatitis
11	1040	100.0	3011	8	ADR29357 Hepatitis
12	1036	99.6	190	7	ADP39661 Hepatitis
13	1036	99.6	215	2	AAR14557 HCV Capsi
14	1036	99.6	215	2	AAR14558 Polypepti
15	1036	99.6	215	2	AAR81945 Hepatitis
16	1036	99.6	215	2	AAR81944 Hepatitis
17	1036	99.6	217	2	AAR70828 Hepatitis
18	1036	99.6	217	2	AAR70829 Insert of
19	1036	99.6	217	2	AAR80517 Insert of
20	1036	99.6	217	2	AAR80516 Hepatitis
21	1035	99.5	190	5	AAB71256 HCV type
22	1035	99.5	191	3	AAY82997 Hepatitis
23	1035	99.5	2955	8	ADN35978 HCV cDNA
24	1031	99.1	191	2	AAR44010 Hepatitis
25	1031	99.1	191	2	AAR92938 Hepatitis

ALIGNMENTS

RESULT 1

AAY82999
ID AAY82999 standard; peptide; 191 AA.

AC AAY82999;

XX 12-SEP-2003 (revised)

DT 04-JUL-2000 (first entry)

DE Hepatitis C virus core polypeptide.

XX Hepatitis C virus; HCV; core polypeptide; antigen; epitope; agrtotope;

KW anchor residue; cytotoxic T lymphocyte; CTL; immune response; MHC;

KW Major histocompatibility complex; vaccine; treatment.

OS Hepatitis C virus; (HCV).

XX WO200011186-A1.

PD 02-MAR-2000.

PF 17-AUG-1999; 99WO-US018674.

PR 21-AUG-1998; 98US-0097446P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Berzofsky JA, Sarobe P, Pendleton CD, Feinstein SM, Arichi T;

Major ME;

DR WPI; 2000-246569/21.

XX Hepatitis C virus polypeptides is useful as a vaccine for treating

PT Hepatitis C virus infection and for activating cytotoxic T lymphocytes.

PS Disclosure; Page 72-73; 78pp; English.

XX Peptide fragments of the Hepatitis C virus (HCV) core polypeptide can be used to elicit an immune response. A cytotoxic T-lymphocyte (CTL) response is present in patients acutely and chronically infected by HCV. CTL's recognise viral antigens as peptides presented by Class I molecules of the major histocompatibility complex (MHC). These peptide antigens are typically 8-10 amino acids long. These peptide antigens typically have a sequence pattern or motif depending upon which particular MHC antigen they are bound and presented by. The motifs are based on the presence in precise positions in the peptide sequence of several amino acids (agrtropic residues) called anchor residues, responsible for interactions between peptide and MHC molecule, as well as other secondary position

CC that may help to stabilise the interaction. Thus, single amino acid
 CC changes within the peptide sequence can enhance the immune response.
 CC Peptides derived from the HCV core polypeptide having substituted amino
 CC acids within their sequence, specifically a hepatitis C virus core
 CC polypeptide comprising an L to an A substitution at amino acid position
 CC 139 enhance the immune response against HCV. They can therefore be used
 CC as a vaccine or for treating HCV infection. (Updated on 12-SEP-2003 to
 CC standardise OS field)

XX
 SQ Sequence 191 AA;
 Query Match 100.0%; Score 1040; DB 3; Length 191;
 Best Local Similarity 100.0%; Pred. No. 1.5e-90;
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNKNTNRPPQDVKFPFGGGQIVGGVYLLPRGRLGVRAATKTSERSQPRG 60
 DB 1 MSTNPKQKKNKNTNRPPQDVKFPFGGGQIVGGVYLLPRGRLGVRAATKTSERSQPRG 60
 QY 61 RRQPIKARRPEGRGRTWAQPGYWPPLYGNECCGAGWLLSPRGSRSRPSWGPTDPRRSRNLG 120
 DB 61 RRQPIKARRPEGRGRTWAQPGYWPPLYGNECCGAGWLLSPRGSRSRPSWGPTDPRRSRNLG 120
 QY 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGVNYATGNLPGCSFSIFLLA 180
 DB 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGVNYATGNLPGCSFSIFLLA 180
 QY 181 LLSCLTVPASA 191
 DB 181 LLSCLTVPASA 191

RESULT 2
 AAR34009
 ID AAR34009 standard; protein; 2816 AA.
 AC AAR34009;
 XX
 XX 25-MAR-2003 (revised)
 DT 26-JUL-1993 (first entry)
 XX
 XX HCV-1 polypeptide.
 XX
 XX Polymerase chain reaction; PCR; amplify; primer; hepatitis C virus; HCV;
 KW asymptomatic; chronically infected; epitope; viral isolate; domain;
 KW immunological; cross-reactive; envelope protein; vaccine;
 KW gp53 (BVDV)/gp55; hog cholera virus; pestivirus; NS1; flavivirus.
 XX
 OS Hepatitis C virus.
 XX
 XX WO9306126-A1.
 XX
 XX 01-APR-1993.
 XX
 XX 11-SEP-1992; 92WO-US007683.
 XX
 XX 13-SEP-1991; 91US-00795975.
 XX
 XX (CHIR) CHIRON CORP.
 XX
 XX Weiner AJ, Houghton M;
 XX
 XX WPI; 1993-117468/14.
 XX
 XX Immuno-reactive hepatitis C virus polypeptide compsns. - contg. at least
 PT 2 sequences from the first variable domain of distinct HCV isolates.
 XX
 XX Disclosure; Fig 9; 106pp; English.
 XX
 XX This sequence represents the entire hepatitis C virus polypeptide. HCV is
 CC a member of the flavivirus family and appears to encode a basic
 CC polypeptide domain ("C") at the N-terminal of the viral polypeptide,
 CC followed by two glycoprotein domains ("E1", "E2/NS1"), upstream of the

CC nonstructural genes NS2 through NS5. See also AAQ39134-48, AAR33982- 4008
 CC and AAR38088-89. (Updated on 25-MAR-2003 to correct PN field.)

XX
 SQ Sequence 2816 AA;
 Query Match 100.0%; Score 1040; DB 2; Length 2816;
 Best Local Similarity 100.0%; Pred. No. 3.1e-89;
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNKNTNRPPQDVKFPFGGGQIVGGVYLLPRGRLGVRAATKTSERSQPRG 60
 DB 1 MSTNPKQKKNKNTNRPPQDVKFPFGGGQIVGGVYLLPRGRLGVRAATKTSERSQPRG 60
 QY 61 RRQPIKARRPEGRGRTWAQPGYWPPLYGNECCGAGWLLSPRGSRSRPSWGPTDPRRSRNLG 120
 DB 61 RRQPIKARRPEGRGRTWAQPGYWPPLYGNECCGAGWLLSPRGSRSRPSWGPTDPRRSRNLG 120
 QY 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGVNYATGNLPGCSFSIFLLA 180
 DB 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGVNYATGNLPGCSFSIFLLA 180
 QY 181 LLSCLTVPASA 191
 DB 181 LLSCLTVPASA 191

RESULT 3
 AAY14975
 ID AAY14975 standard; protein; 2955 AA.
 AC AAY14975;
 XX
 XX 20-MAR-2003 (revised)
 DT 08-NOV-1999 (first entry)
 XX
 XX Amino acid sequence of HCV-1 ORF.
 XX
 XX Hepatitis C virus; HCV; J1; J7; HCV-1; non-A, non-B HCV; NANBH;
 KW HCV infection; vaccine.
 XX
 OS Hepatitis C virus.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 441 /note= "encoded by TT"
 FT Misc-difference 461 /note= "encoded by CCCC"
 XX
 XX EP939128-A2.
 XX
 XX 01-SEP-1999.
 XX
 XX 17-SEP-1990; 99EP-00101746.
 XX
 XX 15-SEP-1989; 89US-00408045.
 PR 21-DEC-1989; 89US-00456142.
 PR 17-SEP-1990; 90EP-00310149.
 XX
 XX (OYAA/) OYA A.
 PA (CHIR) CHIRON CORP.
 XX
 XX Miyamura T, Saito I, Houghton M, Weiner AJ, Han J, Kolberg JA;
 PI Cha T, Irvine BD;
 XX
 XX WPI; 1999-480843/41.
 DR N-PSDB; AA207656.
 XX
 XX New Hepatitis C Virus isolates, useful for diagnosis of hepatitis
 PT infections and development of vaccines.
 XX
 XX Disclosure; Fig 12; 132pp; English.
 XX
 XX The invention provides two new isolates of hepatitis C virus (HCV), J1

CC and J7. These two isolates comprise nucleotide and amino acid sequences
CC that are distinct from the HCV isolate HCV-1. The nucleotide sequences
CC may be used to detect non-A, non-B HCV (NANBH) polynucleotides by
CC hybridisation for diagnosis of NANBH infections. They may also be used to
CC screen blood donors, donated blood and blood products for this infection.
CC The isolates may also be used to isolate other naturally occurring
CC variants of the virus. The polypeptides may be used as a vaccine for
CC administration to patients to protect against infection with NANBH. The
CC present sequence represents the amino acid sequence of HCV-1 ORF.
CC (Updated on 20-MAR-2003 to correct PF field.) (Updated on 20-MAR-2003 to
CC correct PR field.)
XX
XX Sequence 2955 AA;

Query Match 100.0%; Score 1040; DB 2; Length 2955;
Best Local Similarity 100.0%; Pred. No. 3.3e-89;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSTNPKPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRRGLGVRATKTSERSQPRG 60
DB 1 MSTNPKPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRRGLGVRATKTSERSQPRG 60
QY 61 RRQPIPKARRPEGRRTWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSGWPTDPRRSRNLG 120
DB 61 RRQPIPKARRPEGRRTWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSGWPTDPRRSRNLG 120
QY 121 KVIDTLTCGFADLMGYIPLVCGAPLGGAAARALAHGVRLVDGVNATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPLVCGAPLGGAAARALAHGVRLVDGVNATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191

RESULT 4
AAB18541
ID AAB18541 standard; protein; 2955 AA.
XX AC AAB18541;
XX
XX 15-JAN-2001 (first entry)
XX Polypeptide encoded by sense strand of HCV.
XX Hepatitis C virus; HCV; antisense polynucleotide; polypeptide;
XX viral infectivity; viral replication.
XX Hepatitis C virus.
XX EPI034785-A2.
XX
XX 13-SEP-2000.
XX 16-MAR-1990; 2000EP-00109602.
XX 17-MAR-1989; 89US-00325338.
XX 20-APR-1989; 89US-003411334.
XX 18-MAY-1989; 89US-00355002.
XX 16-MAR-1990; 90EP-00302866.
XX (CHIR) CHIRON CORP.
XX Houghton M, Choo Q, Kuo G;
XX WPI; 2000-566891/53.
XX N-PSDB; AAA75297.
XX Novel composition comprising a hepatitis C virus antisense polynucleotide
XX which is complementary to or corresponds to a sense strand of the virus
XX genome, and selectively hybridizes to it.
XX Example; Fig 17; 75pp; English.

XX The specification describes a pharmaceutical composition which comprises
CC a hepatitis C virus (HCV) antisense polynucleotide. The HCV is
CC characterized by a positive stranded RNA genome which has 40% homology at
CC the polypeptide level to a HCV polypeptide. The antisense polynucleotide
CC binds to cellular polynucleotides which enhance and/or are required for
CC viral infectivity, replicative ability or chronicity. The antisense
CC polynucleotides may also be designed to bind with high specificity, to be
CC of increased stability, to be stable and to have low toxicity. The
CC composition also comprises an agent which causes viral RNA to be
CC inactive. The composition is used for preventing HCV replication in a
CC system. The present sequence is encoded by a novel HCV CDNA sequence,
CC which is used in the course of the invention
XX
XX Sequence 2955 AA;

Query Match 100.0%; Score 1040; DB 3; Length 2955;
Best Local Similarity 100.0%; Pred. No. 3.3e-89;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSTNPKPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRRGLGVRATKTSERSQPRG 60
DB 1 MSTNPKPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRRGLGVRATKTSERSQPRG 60
QY 61 RRQPIPKARRPEGRRTWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSGWPTDPRRSRNLG 120
DB 61 RRQPIPKARRPEGRRTWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSGWPTDPRRSRNLG 120
QY 121 KVIDTLTCGFADLMGYIPLVCGAPLGGAAARALAHGVRLVDGVNATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPLVCGAPLGGAAARALAHGVRLVDGVNATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191

RESULT 5
AAR21519
ID AAR21519 standard; protein; 3011 AA.
XX AC AAR21519;
XX
XX 24-OCT-2003 (revised)
XX 25-MAR-2003 (revised)
XX 22-JUN-1992 (first entry)
XX Compiled HCV sequence.
XX HCV1; serum; gt11.
XX Hepatitis C virus type 1.
XX
XX Key Location/Qualifiers
XX Misc-difference 9 /label= ARG
XX Misc-difference 11 /label= THR
XX Misc-difference 176 /label= THR
XX Misc-difference 334 /label= VAL
XX Misc-difference 603 /label= ILE
XX Misc-difference 848 /label= (ASN)
XX Misc-difference 1114 /label= SER
XX Misc-difference 1117 /label= THR
XX Misc-difference 1276 /label= LEU
XX Misc-difference 1328

```

FT      /label= (VAL)
FT Misc-difference 1454
FT      /label= TYR
FT Misc-difference 1471
FT      /label= (SER)
FT Misc-difference 1877
FT      /label= (GLY)
FT Misc-difference 1948
FT      /label= (HIS)
FT Misc-difference 1949
FT      /label= (CYS)
FT Misc-difference 2021
FT      /label= (VAL)
FT Misc-difference 2349
FT      /label= (SER)
FT Misc-difference 2385
FT      /label= (PHE)
FT Misc-difference 2386
FT      /label= (ALA)
FT Misc-difference 2502
FT      /label= (PHE)
FT Misc-difference 2690
FT      /label= (GLY)
FT Misc-difference 2996
FT      /label= (PRO)
XX
XX WO9202642-A.
XX
XX 20-FEB-1992.
XX
XX 10-AUG-1990; 90US-00566209.
XX
XX 10-AUG-1990; 90US-00566209.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Houghton M, Choo QL, Kuo G, Weiner AJ, Ureda MS, Irvine BD;
XX Kolberg JA;
XX
XX WPI; 1992-080094/10.
XX N-PSDB; AAQ21744.
XX
XX Reagents for isolating, amplifying and detecting HCV polynucleotide(s) -
XX used to monitor spread of blood-borne non-a, non-b hepatitis virus
XX infection and screen blood samples for virus.
XX
XX Disclosure; Fig 1; 67pp; English.
XX
XX Heterogeneities in cloned DNAs of HCV1 are indicated by the amino acid
XX indicated in the features, the parentheses indicated that the
XX heterogeneity was detected at or near to the 5'- or 3'-end of the HCV in
XX the clone. The sequence is derived from a composite HCV cDNA from HCV1, a
XX prototypic HCV. The DNA sequence is based upon sequence information
XX derived from a no. of HCV cDNA clones, which were isolated from a no. of
XX HCV cDNA libraries, including the "c" library present in lambda gt11
XX (ATCC No.40394), and from human serum. The HCV cDNA clones were isolated
XX by methods described in WO9014436. The clones from which the sequence was
XX derived are 5'clone32, b114a, 18g, ag30a, CA205a, CA290a, CA216a, p14a,
XX CA167b, CA156e, CA84a, CA59a, K9-1 (also called k9-1), 26j, 13i, 12f,
XX 14i, 11b, 7f, 7e, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c, 14c, 8f,
XX 33f, 33g, 39c, 35f, 19g, 26g, 15e, b5a, 16ih, 6k and p131jh. (Updated on
XX 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
XX field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
XX Sequence 3011 AA;
XX
XX Query Match 100.0%; Score 1040; DB 2; Length 3011;
XX Best Local Similarity 100.0%; Pred. No. 3.4e-89;
XX Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MSTNPKPKKNTNRNPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60
XX      |||||
XX 1 MSTNPKPKKNTNRNPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60

```

```

QY      61 RRQPIKARRPRGRTWAORGYDPLVGNEGCGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120
Db      |||||
Db      61 RRQPIKARRPRGRTWAORGYDPLVGNEGCGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120
QY      121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db      |||||
Db      121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
QY      181 LLSCLTVPASA 191
Db      |||||
Db      181 LLSCLTVPASA 191

RESULT 6
AAR90931
ID AAR90931 standard; protein; 3011 AA.
XX
XX AAR90931;
XX
XX 25-MAR-2003 (revised)
DT 15-MAY-1996 (first entry)
XX
XX Hepatitis C virus polyprotein.
DE
XX
XX Non-A non-B hepatitis virus; NANBHV; HCV; antigen; detection; diagnosis;
XX antibodies.
XX
XX Hepatitis C virus.
XX
XX Key Location/Qualifiers
FT Misc-difference 1..122 /label= antigen
FT /note= "C22; AAR90936"
FT Misc-difference 199..328 /label= antigen
FT /note= "S2; AAR90935"
FT Misc-difference 1192..1457 /label= antigen
FT /note= "C33c; AAR90932"
FT Misc-difference 1569..1931 /label= antigen
FT /note= "C100; AAR90933"
FT Misc-difference 2054..2464 /label= antigen
FT /note= "NS5; AAR90934"
XX
XX EP693687-A1.
XX
XX 24-JAN-1996.
XX
XX 03-APR-1991; 95EP-00114016.
XX
XX 04-APR-1990; 90US-00504352.
XX (CHIR ) CHIRON CORP.
XX
XX Houghton M, Choo Q, Kuo G;
XX WPI; 1996-117956/13.
XX N-PSDB; AAT12710.
XX
XX Combinations of synthetic Hepatitis C Virus antigens - provide more
XX effective diagnosis of Non-A, Non-B Hepatitis.
XX
XX Disclosure; Fig 1(A-Y); 53pp; English.
XX
XX The combination comprises an HCV antigen from the C domain (pref. C22 -
XX AAR90936) and at least one HCV antigen from the NS3 (pref. C33c -
XX AAR90932), NS4 (pref. C100 - AAR90933), S (pref. S2 - AAR90935) or NS5
XX (AAR90934) domain. The antigens may in the form of a fusion protein, a
XX simple physical mixture, or the individual antigens commonly bound to a
XX solid matrix. They are pref. prepd. by recombinant DNA techniques

```

CC	(primers are given in AAT12711-T12716), but can be synthesised or
CC	isolated from HCV using affinity chromatography. (Updated on 25-MAR-2003
CC	to correct PF field.)
XX	
SQ	Sequence 3011 AA;
	Query Match 100.0%; Score 1040; DB 2; Length 3011;
	Best Local Similarity 100.0%; Pred. No. 3.4e-89;
	Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MSTNPKPQKKNTNRPPDVKFPGGQIVGGVLLPRGPRLGVRAKTKTSERSOPRG 60
DB	1 MSTNPKPQKKNTNRPPDVKFPGGQIVGGVLLPRGPRLGVRAKTKTSERSOPRG 60
QY	61 RRPIPKARRPEGRITWAPGYWPPLYNGEGCGAGWLLSPRGSRPSPMGPTDPRRSRNLG 120
DB	61 RRPIPKARRPEGRITWAPGYWPPLYNGEGCGAGWLLSPRGSRPSPMGPTDPRRSRNLG 120
QY	121 KVIDTLTCGFADLMGYIPLVGAPIGGGAARALAHGVRLVEDGVNVTATGNLPCGCSFSIFLLA 180
DB	121 KVIDTLTCGFADLMGYIPLVGAPIGGGAARALAHGVRLVEDGVNVTATGNLPCGCSFSIFLLA 180
QY	181 LLSCLTVPASA 191
DB	181 LLSCLTVPASA 191
RESULT 7	
AAW34480	
ID	AAW34480 standard; protein; 3011 AA.
XX	AAW34480;
XX	
DT	25-MAR-2003 (revised)
DT	16-MAR-1998 (first entry)
XX	
DE	HCV polyprotein.
XX	
KW	PCR primer; amplify; HCV; hepatitis c virus; antigen combination; NS3;
KW	C domain; S domain; NSS; HCV polyprotein; anti-HCV antibody; detection;
KW	NS4.
XX	
OS	Hepatitis C virus.
XX	
FH	Location/Qualifiers
FT	Misc-difference /note= "can optionally be Arg"
FT	Misc-difference 372 /note= "can optionally be Thr"
FT	Misc-difference 867 /note= "can optionally be Thr"
FT	Misc-difference 1341 /note= "can optionally be Val"
FT	Misc-difference 2148 /note= "can optionally be Ile"
FT	Misc-difference 2883 /note= "can optionally be Asn"
FT	Misc-difference 3681 /note= "can optionally be Ser"
FT	Misc-difference 3690 /note= "can optionally be Thr"
FT	Misc-difference 4167 /note= "can optionally be Leu"
FT	Misc-difference 4323 /note= "can optionally be Val"
FT	Misc-difference 4701 /note= "can optionally be Tyr"
FT	Misc-difference 4752 /note= "can optionally be Ser"
FT	Misc-difference 5970 /note= "can optionally be Gly"
FT	Misc-difference 6183 /note= "can optionally be His"
FT	

```
Db      1  MSTNPKQKKNKNTNRRPDVKFPGGQIVGGVYLLPRGPRILGVRAHKTTSERSQPRG 60
Qy      61  RROPIPKARPEGRTHAQPGYPWPLVYNECGWAGWLLSPRGSRPSWGTDPDRRSRNLG 120
        |||||
Db      61  RROPIPKARPEGRTHAQPGYPWPLVYNECGWAGWLLSPRGSRPSWGTDPDRRSRNLG 120
        |||||
Qy      121  KVDTLTTCGADLMGVIPLVYCAPLGGGAARALAHGVRLVDGVNATGNLPGCSFSIFLLA 180
        |||||
Db      121  KVDTLTTCGADLMGVIPLVYCAPLGGGAARALAHGVRLVDGVNATGNLPGCSFSIFLLA 180
        |||||
Qy      181  LLSCLTVPASA 191
        |||||
Db      181  LLSCLTVPASA 191
        |||||

RESULT 8
AAW40038
ID      AAW40038 standard; protein; 3011 AA.
XX
AC      AAW40038;
XX
DT      26-MAY-1998 (first entry)
XX
DE      HCV polyprotein.
XX
KW      Hepatitis C virus C domain; HCV; C antigen; immunological activity;
KW      NS3 domain; NS4 domain; S domain; NS5 domain.
XX
OS      Hepatitis C virus.
XX
FH      Location/Qualifiers
FT      Domain
          1..120
          /label= C_domain
FT      Modified-site
          9
          /note= "As given in the specification this amino acid can
          also be Arg"
FT      Modified-site
          11
          /note= "As given in the specification this amino acid can
          also be Thr"
FT      Domain
          120..400
          /label= S_domain
FT      Modified-site
          174
          /note= "As given in the specification this amino acid can
          also be Thr"
FT      Modified-site
          334
          /note= "As given in the specification this amino acid can
          also be Val"
FT      Modified-site
          603
          /note= "As given in the specification this amino acid can
          also be Ile"
FT      Modified-site
          847
          /note= "As given in the specification this amino acid can
          also be Asn"
FT      Domain
          1050..1640
          /label= NS3_domain
FT      Modified-site
          1114
          /note= "As given in the specification this amino acid can
          also be Ser"
FT      Modified-site
          1217
          /note= "As given in the specification this amino acid can
          also be Thr"
FT      Modified-site
          1276
          /note= "As given in the specification this amino acid can
          also be Leu"
FT      Modified-site
          1328
          /note= "As given in the specification this amino acid can
          also be Val"
FT      Modified-site
          1452
          /note= "As given in the specification this amino acid can
          also be Tyr"
FT      Modified-site
          1472
          /note= "As given in the specification this amino acid can
          also be Ser"
```

```
FT      Domain
          1640..2000
          /label= NS4_domain
FT      Modified-site
          1877
          /note= "As given in the specification this amino acid can
          also be Gly"
FT      Modified-site
          1948
          /note= "As given in the specification this amino acid can
          also be His"
FT      Modified-site
          1949
          /note= "As given in the specification this amino acid can
          also be Cys"
FT      Domain
          2000..3011
          /label= NS5_domain
FT      Modified-site
          2021
          /note= "As given in the specification this amino acid can
          also be Val"
FT      Modified-site
          2348
          /note= "As given in the specification this amino acid can
          also be Ser"
FT      Modified-site
          2385
          /note= "As given in the specification this amino acid can
          also be Phe"
FT      Modified-site
          2386
          /note= "As given in the specification this amino acid can
          also be Ala"
FT      Modified-site
          2502
          /note= "As given in the specification this amino acid can
          also be Phe"
FT      Modified-site
          2690
          /note= "As given in the specification this amino acid can
          also be Gly"
FT      Modified-site
          2921
          /note= "As given in the specification this amino acid can
          also be Gly"
FT      Modified-site
          2996
          /note= "As given in the specification this amino acid can
          also be Pro"
XX      US5712087-A.
XX
PD      27-JAN-1998.
XX
PF      12-MAY-1995; 95US-00440519.
XX
PR      04-APR-1990; 90US-00504352.
XX      07-JUL-1992; 92US-00910760.
XX      (CHIR ) CHIRON CORP.
XX      Kuo G, Houghton M, Choo Q;
XX      WPI; 1998-119973/11.
DR      N-PSDB; AAV09989.
XX
PT      Immunoassays for hepatitis C virus antibodies - using combinations of
PT      antigenic fragments of HCV polyprotein.
XX
PS      Disclosure; Fig 1; 59pp; English.
XX
CC      This sequence represents the hepatitis C virus (HCV) polyprotein which is
CC      used in the construction of novel combinations of HCV antigens that have
CC      a broader range of immunological activity than any single HCV antigen. An
CC      example of such an antigen given in this specification comprises a first
CC      antigen containing at least 8 amino acids of the C domain of the HCV
CC      polyprotein and a second antigen comprising at least 8 amino acids of the
CC      NS3 domain, the NS4 domain, the S domain or the NS5 domain of the HCV
CC      polyprotein in the form of a fusion protein, a physical mixture or bound
CC      to a solid matrix. Note: The features given in the specification as
CC      represented in the feature table of AAW40038 differ from the positions
CC      indicated in Figure 1
XX      Sequence 3011 AA;
```

```
Query Match      100.0%; Score 1040; DB 2; Length 3011;
Best Local Similarity 100.0%; Pred. No. 3.4e-89;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60

Qy 61 RROPIKARRPEGRTPAQPGYPWPLYGNECGWAGWLLSPRGRPSWGPTDPRRRRNLG 120
Db 61 RROPIKARRPEGRTPAQPGYPWPLYGNECGWAGWLLSPRGRPSWGPTDPRRRRNLG 120

Qy 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 9
AAE22049
ID AAE22049 standard; protein; 3011 AA.
XX
AC AAE22049;
XX
DT 16-JUL-2002 (first entry)
XX
DE Hepatitis C virus (HCV) polyprotein.
XX
KW Hepatitis C virus; HCV; antigen; C domain; polyprotein; NS3 domain;
KW NS4 domain; S domain; NS5 domain.
XX
OS Hepatitis C virus.
XX
PH Key Location/Qualifiers
FT Domain 1..122
FT Domain /label= C_domain
FT Domain 199..328
FT Domain /label= S_domain
FT Region 1192..1931
FT Region /note= "c200 polypeptide"
FT Region 1192..1457
FT Region /note= "NS3 domain antigen"
FT Region 1569..1931
FT Region /note= "NS4 antigen"
FT Region 2054..2464
FT Region /note= "NS5 antigen"
XX
XX US6312889-B1.
XX
XX
XX 06-NOV-2001.
XX
XX 12-MAY-1995; 95US-00440549.
XX
XX 04-APR-1990; 90US-00504352.
XX 07-JUL-1992; 92US-00910760.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Houghton M, Choo Q, Kuo G;
XX
XX WPI; 2002-040268/05.
XX N-PSDB; AAD35043.
XX
XX Combination of hepatitis C viral (HCV) antigens, useful in improved
XX immunoassay for detecting HCV antibodies.
XX
XX Example 1; Col 45-60; 58pp; English.
XX
XX The invention relates to combination of hepatitis C viral (HCV) antigens
XX that have a broader range of immunological reactivity than any single HCV
```

```
CC antigen. The combinations consist of an antigen from the C domain of the
CC HCV polyprotein, and at least one additional HCV antigen from either the
CC NS3 domain, the NS4 domain, the S domain, or the NS5 domain and are in
CC the form of fusion protein, a simple physical mixture, or the individual
CC antigens commonly bound to a solid matrix. The combinations of antigens
CC provides broad range immunoassays for anti-HCV antibodies. The invention
CC therefore provides a method for detecting antibodies to HCV in a mammal
CC suspected of containing such antibodies. The present sequence is HCV
CC polyprotein. Note: This sequence SEQ.ID.NO:10 is stated to be similar to
CC the sequence shown in Fig 1 (AAE22052) of the specification. However
CC these sequences differ
XX
XX SQ Sequence 3011 AA;
XX
XX Query Match      100.0%; Score 1040; DB 5; Length 3011;
XX Best Local Similarity 100.0%; Pred. No. 3.4e-89;
XX Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60
XX Db 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60
XX
XX Qy 61 RROPIKARRPEGRTPAQPGYPWPLYGNECGWAGWLLSPRGRPSWGPTDPRRRRNLG 120
XX Db 61 RROPIKARRPEGRTPAQPGYPWPLYGNECGWAGWLLSPRGRPSWGPTDPRRRRNLG 120
XX
XX Qy 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
XX Db 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
XX
XX Qy 181 LLSCLTVPASA 191
XX Db 181 LLSCLTVPASA 191
XX
XX RESULT 10
XX ADL23107
XX ID ADL23107 standard; protein; 3011 AA.
XX
XX AC ADL23107;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Hepatitis C virus protein sequence SeqID 2.
XX
XX KW hepatitis C virus; HCV; viral envelope; E2 glycoprotein;
XX KW low density lipoprotein; LDL; HCV infection; hypercholesterolaemia;
XX KW hyperlipidaemia; coronary heart disease; hepatotropic; virucidal;
XX KW plasma lipoprotein.
XX
XX OS Hepatitis C virus.
XX
XX PN WO2004003141-A2.
XX
XX PD 08-JAN-2004.
XX
XX PF 24-JUN-2003; 2003WO-US019834.
XX
XX PR 28-JUN-2002; 2002US-0392158P.
XX 27-MAY-2003; 2003US-00445724.
XX
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX
XX FI Stapleton JT, Wuenschmann S;
XX
XX DR WPI; 2004-083029/08.
XX N-PSDB; ADL23106.
XX
XX PT Use of Hepatitis C Virus E2 glycoprotein in reducing low density
XX PT lipoprotein levels in a subject or in treating or preventing hepatitis C
XX PT virus infection.
XX
XX PS Disclosure; SEQ ID NO 2; 135pp; English.
```



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XX PN WO9115516-A.
XX XX
XX PD 17-OCT-1991.
XX XX
XX PF 06-APR-1990; 90US-00505611.
XX XX
XX PR 06-APR-1990; 90US-00505611.
XX PR 09-OCT-1990; 90US-00594854.
XX XX
XX PA (GENE-) GENELABS INC.
XX XX
XX PI Reyes G, Kim JP, Moeckli R, Simonsen CC;
XX XX
XX DR WPI; 1991-325174/44.
XX DR N-PSDB; AAQ14280.
XX XX
XX PT Hepatitis C virus epitope(s) immuno-reactive with HCV infected sera
XX PT - useful for detection of HCV infections and as HCV vaccine.
XX PS
XX PS Claim 14; Fig 8B; 150pp; English.
XX XX
XX CC Putative HCV capsid protein clones were identified by immunoscreening.
XX CC Clone 56 was sequenced and found to include a run of adenine residues
XX CC around nucleotides 25 to 34; such sequences are similar to sequences
XX CC known to promote translation frameshifting. To improve expression of the
XX CC HCV capsid protein the putative region of frameshifting was modified
XX CC (i.e. adenine residues at the third position of a codon were changed to
XX CC guanines) to give pGEX-CapA. See AAQ14279 for the unmodified clone 56
XX CC sequence. (Updated on 24-OCT-2003 to standardise OS field)
XX XX
XX SQ Sequence 215 AA;

Query Match 99.6%; Score 1036; DB 2; Length 215;
Best Local Similarity 99.5%; Pred. No. 4e-90;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNTNRRPDQVFPGGQIVGGVYLLPRGPRLGVRAATKTSERSQPRG 60
DB 1 MGTNPKQKKNTNRRPDQVFPGGQIVGGVYLLPRGPRLGVRAATKTSERSQPRG 60
QY 61 RRQIPKARRPEGRTWAQGYPPWLYGNEGCWAGWLLSPRGRPSWGPTDPRRRRNLG 120
DB 61 RRQIPKARRPEGRTWAQGYPPWLYGNEGCWAGWLLSPRGRPSWGPTDPRRRRNLG 120
QY 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191

RESULT 15
AAR81945
ID AAR81945 standard; protein; 215 AA.
XX AC
XX AC AAR81945;
XX DT 16-OCT-2003 (revised)
XX DT 23-MAR-2003 (revised)
XX DT 28-JUL-1996 (first entry)
XX XX
XX DE Hepatitis C virus antigen.
XX XX
XX KW Hepatitis C virus; HCV; antigen; detection; diagnosis; vaccine;
XX KW antibodies; immunophylaxis; sera; serum.
XX OS
XX OS Hepatitis C virus; (Clone CapA).
XX PN
XX PN US5443965-A.

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PD XX 22-AUG-1995.
PF XX 05-APR-1991; 91US-00681703.
XX XX
PR 06-APR-1990; 90US-00505611.
PR 09-OCT-1990; 90US-00594854.
XX XX
XX PA (GENE-) GENELABS INC.
XX XX
XX PI Moeckli R, Reyes GR, Kim JP;
XX XX
XX DR WPI; 1995-302120/39.
XX DR N-PSDB; AAQ98208.
XX XX
XX PT New nucleic acids encoding hepatitis C virus antigens - used to develop
XX PT prods. for detection of HCV-infected sera and prodn. of vaccines and anti
XX PT -HCV antibodies.
XX PS
XX PS Disclosure; Col 71-72; 71pp; English.
XX XX
XX CC Hepatitis C virus (HCV) antigens can be used for detecting HCV infected
XX CC sera and individuals infected with HCV. They can also be used in an anti-
XX CC HCV vaccine or for the production of anti-HCV antibodies which can be
XX CC used for passive immunophylaxis. The antigens consistently identify
XX CC more HCV positive serum samples with a high degree of specificity. See
XX CC AAQ98202-14 and AAR81939-51. (Updated on 25-MAR-2003 to correct PF
XX CC field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 16-OCT-
XX CC 2003 to standardise OS field)
XX XX
XX SQ Sequence 215 AA;

Query Match 99.6%; Score 1036; DB 2; Length 215;
Best Local Similarity 99.5%; Pred. No. 4e-90;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNTNRRPDQVFPGGQIVGGVYLLPRGPRLGVRAATKTSERSQPRG 60
DB 1 MGTNPKQKKNTNRRPDQVFPGGQIVGGVYLLPRGPRLGVRAATKTSERSQPRG 60
QY 61 RRQIPKARRPEGRTWAQGYPPWLYGNEGCWAGWLLSPRGRPSWGPTDPRRRRNLG 120
DB 61 RRQIPKARRPEGRTWAQGYPPWLYGNEGCWAGWLLSPRGRPSWGPTDPRRRRNLG 120
QY 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191

Search completed: August 19, 2005, 12:39:28
Job time : 118.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 19, 2005, 12:31:50 ; Search time 110 seconds
(without alignments)

889.156 Million cell updates/sec

Title: US-10-770-117-2

Perfect score: 1040

Sequence: 1 MSTNPKQKKNKNTNRPO.....CSFSIFLLALLSCLTVPASA 191

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1035	99.5	3011	1	POLG_HCV1
2	1026	98.7	191	2	Q68113 hepatitis c
3	1026	98.7	191	2	Q68123 hepatitis c
4	1026	98.7	191	2	Q68124 hepatitis c
5	1026	98.7	191	2	Q68139 hepatitis c
6	1026	98.7	191	2	Q68149 hepatitis c
7	1026	98.7	191	2	Q6QY91 hepatitis c
8	1026	98.7	191	2	Q6QY92 hepatitis c
9	1026	98.7	191	2	Q6QY99 hepatitis c
10	1026	98.7	191	2	Q6QY91 hepatitis c
11	1026	98.7	191	2	Q6QY92 hepatitis c
12	1026	98.7	191	2	Q6QY96 hepatitis c
13	1026	98.7	191	2	Q6QY97 hepatitis c
14	1026	98.7	191	2	Q6QY98 hepatitis c
15	1026	98.7	191	2	Q6QY99 hepatitis c
16	1026	98.7	191	2	Q6QY94 hepatitis c
17	1026	98.7	191	2	Q6QY96 hepatitis c
18	1026	98.7	191	2	Q6QY97 hepatitis c
19	1026	98.7	191	2	Q6QY98 hepatitis c
20	1026	98.7	191	2	Q6QY99 hepatitis c
21	1026	98.7	191	2	Q6QY91 hepatitis c
22	1026	98.7	191	2	Q6QY92 hepatitis c
23	1026	98.7	191	2	Q6QY93 hepatitis c
24	1026	98.7	191	2	Q6QY95 hepatitis c
25	1026	98.7	191	2	Q6QY96 hepatitis c
26	1026	98.7	191	2	Q6QY97 hepatitis c
27	1026	98.7	191	2	Q6QY98 hepatitis c
28	1026	98.7	191	2	Q6QY99 hepatitis c
29	1026	98.7	191	2	Q6QY91 hepatitis c
30	1026	98.7	191	2	Q6QY92 hepatitis c
31	1026	98.7	191	2	Q6QY93 hepatitis c

Q6QYF6 hepatitis c
Q6QYF7 hepatitis c
Q6QYF9 hepatitis c
Q6QY90 hepatitis c
Q6QY95 hepatitis c
Q6QY97 hepatitis c
Q6QY99 hepatitis c
Q6QYK0 hepatitis c
Q6QYK2 hepatitis c
Q6QYK3 hepatitis c
Q6QYK6 hepatitis c
Q6QYK7 hepatitis c
Q6QYK8 hepatitis c
Q6QYK9 hepatitis c

ALIGNMENTS

RESULT 1

POLG_HCV1 STANDARD; PRT; 3011 AA.
AC P26664; 1026 98.7 191 2 Q6QYF6
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Genome polyprotein [Contains: Capsid protein C (Core protein) (P22); Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21) (EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepatitis C virus) (EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
DE Hepatitis C virus (isolate 1) (HCV).
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepatitis C virus.
OC Hepatitis C virus.
OX NCBI_TaxID=11104;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91172826; PubMed=1848704;
RA Choo Q.-L., Richman K.H., Han J.H., Berger K., Lee C., Dong C., Gallegos C., Colt D., Medina-Selby A., Barr P.J., Weiner A.J., Bradley D.W., Kuo G., Houghton M.;
RA "Genetic organization and diversity of the hepatitis C virus.";
Proc. Natl. Acad. Sci. U.S.A. 88:2451-2455(1991).
CC -I- FUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are hydrophobic, suggesting a possible membrane-related function. NS3 and NS5 may play a role in the viral RNA replication.
CC -I- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral precursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'.
CC -I- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + {RNA}(N).
CC -I- SUBUNIT: The virion of this virus is a nucleocapsid covered by a lipoprotein envelope. The envelope consists of two proteins: protein M and glycoprotein E. The nucleocapsid is a complex of protein C and mRNA.
CC -I- SIMILARITY: Contains 1 peptidase S29 domain.
CC -I- SIMILARITY: Contains 1 peptidase U39 domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announcements or send an email to license@isb-sib.ch).
CC EMBL: M62321; AAA45676.1; -
DR PIR: A39166; GNVWC3.
DR PDB: 1HEI; X-ray; A/B=1206-1656.
DR PDB: 1ONB; NMR; A=1349-1507.
DR MEROPS: S29.001; -.


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RP SEQUENCE FROM N.A.
RX MEDLINE=93376778; PubMed=8396266;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "At least 12 genotypes of hepatitis C virus predicted by sequence
RL analysis of the putative E1 gene of isolates collected worldwide.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8234-8238(1993).
DR EMBL; U10232; AAA21071.1; -.
DR PIR; PQ0804; PQ0804.
DR HSSP; O8JVS1; ICWX.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
KW Polyprotein.
FT CHAIN 1 >191 core protein.
FT NON TER 191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 98.7%; Score 1026; DB 2; Length 191;
Best Local Similarity 98.4%; Pred. No. 2e-78;
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNRNTNRRPQDVKPGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60
Db 1 MSTNPKQKKNRNTNRRPQDVKPGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

Qy 61 RRQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGSRRPSWGPTDPRRRSRNLG 120
Db 61 RRQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGSRRPSWGPTDPRRRSRNLG 120

Qy 121 KVDTLTTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVDTLTTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 7
Q6QY91 ID Q6QY91 PRELIMINARY; PRT; 191 AA.
AC Q6QY91;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sherman K.E., Qin H., Shire N., Rousster S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY522326; AAS15488.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
FT NON TER 191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 98.7%; Score 1026; DB 2; Length 191;
Best Local Similarity 98.4%; Pred. No. 2e-78;
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNRNTNRRPQDVKPGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60
Db 1 MSTNPKQKKNRNTNRRPQDVKPGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

Qy 61 RRQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGSRRPSWGPTDPRRRSRNLG 120
Db 61 RRQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGSRRPSWGPTDPRRRSRNLG 120

Qy 121 KVDTLTTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVDTLTTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 9
Q6QY99 ID Q6QY99 PRELIMINARY; PRT; 191 AA.
AC Q6QY99;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sherman K.E., Qin H., Shire N., Rousster S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY522326; AAS15488.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
FT NON TER 191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 98.7%; Score 1026; DB 2; Length 191;
Best Local Similarity 98.4%; Pred. No. 2e-78;
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNRNTNRRPQDVKPGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60
Db 1 MSTNPKQKKNRNTNRRPQDVKPGGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

Qy 61 RRQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGSRRPSWGPTDPRRRSRNLG 120
Db 61 RRQPIPKARRPEGRRTWAQPGYPMPLYGNECGWAGWLLSPRGSRRPSWGPTDPRRRSRNLG 120

Qy 121 KVDTLTTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVDTLTTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

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OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sherman K.E., Qin H., Shire N., Rouster S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY522318; AAS15480.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
FT NON TER 191_191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 98.7%; Score 1026; DB 2; Length 191;
Best Local Similarity 98.4%; Pred. No. 2e-78;
Matches 188; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 MSTNPKQKKNTNRPPQDVKFGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKPQRTKNTNRPPQDVKFGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Qy 61 RROPIKARPEGRTPAQGPWPPLYGNECGWAGLLSPRGRPSWGPTDPRRRSRNLG 120
Db 61 RROPIKARPEGRTPAQGPWPPLYGNECGWAGLLSPRGRPSWGPTDPRRRSRNLG 120
Qy 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPVPLVGAFLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 10
Q6QYAL ID Q6QYAL PRELIMINARY; PRT; 191 AA.
AC Q6QYAL;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sherman K.E., Qin H., Shire N., Rouster S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY522315; AAS15477.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
FT NON TER 191_191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 98.7%; Score 1026; DB 2; Length 191;
Best Local Similarity 98.4%; Pred. No. 2e-78;
Matches 188; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 MSTNPKQKKNTNRPPQDVKFGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKPQRTKNTNRPPQDVKFGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Qy 61 RROPIKARPEGRTPAQGPWPPLYGNECGWAGLLSPRGRPSWGPTDPRRRSRNLG 120
Db 61 RROPIKARPEGRTPAQGPWPPLYGNECGWAGLLSPRGRPSWGPTDPRRRSRNLG 120
Qy 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPVPLVGAFLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 11
Q6QYA2 ID Q6QYA2 PRELIMINARY; PRT; 191 AA.
AC Q6QYA2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sherman K.E., Qin H., Shire N., Rouster S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY522315; AAS15477.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
FT NON TER 191_191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 98.7%; Score 1026; DB 2; Length 191;
Best Local Similarity 98.4%; Pred. No. 2e-78;
Matches 188; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 MSTNPKQKKNTNRPPQDVKFGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKPQRTKNTNRPPQDVKFGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Qy 61 RROPIKARPEGRTPAQGPWPPLYGNECGWAGLLSPRGRPSWGPTDPRRRSRNLG 120
Db 61 RROPIKARPEGRTPAQGPWPPLYGNECGWAGLLSPRGRPSWGPTDPRRRSRNLG 120
Qy 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPVPLVGAFLGGAAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 12
Q6QYA6 ID Q6QYA6 PRELIMINARY; PRT; 191 AA.
AC Q6QYA6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sherman K.E., Qin H., Shire N., Rouster S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY522316; AAS15478.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
FT NON TER 191_191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 98.7%; Score 1026; DB 2; Length 191;
Best Local Similarity 98.4%; Pred. No. 2e-78;
Matches 188; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 MSTNPKQKKNTNRPPQDVKFGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKPQRTKNTNRPPQDVKFGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Qy 61 RROPIKARPEGRTPAQGPWPPLYGNECGWAGLLSPRGRPSWGPTDPRRRSRNLG 120
Db 61 RROPIKARPEGRTPAQGPWPPLYGNECGWAGLLSPRGRPSWGPTDPRRRSRNLG 120
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DR EMBL; AY522311; AAS15473.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
FT NON_TER 191_191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 98.7%; Score 1026; DB 2; Length 191;
Best Local Similarity 98.4%; Pred. No. 2e-78;
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNTNRRPQDVKPPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60
Db 1 MSTNPKPQRTKNTNRRPQDVKPPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

Qy 61 RROPIPKARRPEGRTPAQPGYPWPLYNCGWAGWLLSPRGRPSWGPTDPRRRSRNLG 120
Db 61 RROPIPKARRPEGRTPAQPGYPWPLYNCGWAGWLLSPRGRPSWGPTDPRRRSRNLG 120

Qy 121 KVDTLTGCFADLMGYIPAVGAPLGGAAALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
Db 121 KVDTLTGCFADLMGYIPAVGAPLGGAAALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 13
Q6QYA7 PRELIMINARY; PRT; 191 AA.
ID Q6QYA7
AC Q6QYA7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SHERMAN K.E., QIN H., SHIRE N., ROUSTER S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY522310; AAS15472.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
FT NON_TER 191_191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 98.7%; Score 1026; DB 2; Length 191;
Best Local Similarity 98.4%; Pred. No. 2e-78;
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNTNRRPQDVKPPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60
Db 1 MSTNPKPQRTKNTNRRPQDVKPPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

Qy 61 RROPIPKARRPEGRTPAQPGYPWPLYNCGWAGWLLSPRGRPSWGPTDPRRRSRNLG 120
Db 61 RROPIPKARRPEGRTPAQPGYPWPLYNCGWAGWLLSPRGRPSWGPTDPRRRSRNLG 120

Qy 121 KVDTLTGCFADLMGYIPAVGAPLGGAAALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
Db 121 KVDTLTGCFADLMGYIPAVGAPLGGAAALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 14
Q6QYB1 PRELIMINARY; PRT; 191 AA.
ID Q6QYB1
AC Q6QYB1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SHERMAN K.E., QIN H., SHIRE N., ROUSTER S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY522306; AAS15468.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
FT NON_TER 191_191
SQ SEQUENCE 191 AA; 20766 MW; 4506596F21B4A893 CRC64;

Query Match 98.7%; Score 1026; DB 2; Length 191;
Best Local Similarity 98.4%; Pred. No. 2e-78;
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNTNRRPQDVKPPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60
Db 1 MSTNPKPQRTKNTNRRPQDVKPPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

Qy 61 RROPIPKARRPEGRTPAQPGYPWPLYNCGWAGWLLSPRGRPSWGPTDPRRRSRNLG 120
Db 61 RROPIPKARRPEGRTPAQPGYPWPLYNCGWAGWLLSPRGRPSWGPTDPRRRSRNLG 120

Qy 121 KVDTLTGCFADLMGYIPAVGAPLGGAAALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
Db 121 KVDTLTGCFADLMGYIPAVGAPLGGAAALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 15
Q6QYB2 PRELIMINARY; PRT; 191 AA.
ID Q6QYB2
AC Q6QYB2
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SHERMAN K.E., QIN H., SHIRE N., ROUSTER S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY522305; AAS15467.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
```


Db	1	MSTNPKQKKNKNTNRRPDQVFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
Qy	61	RRQPIPKARRPEGRTWAOQGYPMPLYGNECGWAGLLSPRGSRPSWGPTDPRRRSRNLG 120
Db	61	RRQPIPKARRPEGRTWAOQGYPMPLYGNECGWAGLLSPRGSRPSWGPTDPRRRSRNLG 120
Qy	121	KVIDTLTCGFADLMGYIPAVGAPLGGNARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
Db	121	KVIDTLTCGFADLMGYIPLVGAPLGGNARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
Qy	181	LLSCLTVPASA 191
Db	181	LLSCLTVPASA 191
RESULT 2		
GNWVCH		
genome polyprotein - hepatitis C virus (strain H)		
N;Contains: capsid protein C; envelope protein M; hepatitis virus (EC 3.4.21.98) (nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5		
C;Species: hepatitis C virus		
A;Note: host Homo sapiens (man)		
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004		
A;Accession: A36814; A41546		
R;Inchauspe, G.; Zebedes, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.		
submitted to GenBank, July 1992		
A;Description: Genomic structure of the human prototype strain H of hepatitis C virus: C		
A;Reference number: A36814		
A;Accession: A36814		
A;Molecule type: genomic RNA		
A;Residues: 1-3011 <INC>		
A;Cross-references: UNIPROT:P27958; GB:M67463; NID:G329737; PIDN:AAA45534.1; PID:G329738		
R;Inchauspe, G.; Zebedes, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.		
Proc. Natl. Acad. Sci. U.S.A. 88, 10292-10296, 1991		
A;Title: Genomic structure of the human prototype strain H of hepatitis C virus: compar		
A;Reference number: A41546; MUID:92052256; PMID:1658800		
A;Contents: annotation		
A;Note: neither amino acid nor nucleotide sequence is given		
C;Superfamily: hepatitis C virus genome polyprotein		
C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructural		
F;1-115/Product: capsid protein C #status predicted <CPC>		
F;116-191/Product: envelope protein M #status predicted <EPM>		
F;192-389/Product: major envelope protein E #status predicted <MEE>		
F;390-729/Product: nonstructural protein NS1 #status predicted <NS1>		
F;730-1006/Product: nonstructural protein NS2 #status predicted <NS2>		
F;1007-1615/Product: hepatitis virus #status predicted <NS3>		
F;1230-1237/Region: nucleotide-binding motif A (P-loop)		
F;1312-1317/Region: nucleotide-binding motif B		
F;1316-1319/Region: DEXH motif		
F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4a>		
F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4b>		
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>		
F;196,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2240,23		
Query Match 98.78; Score 1026; DB 1; Length 3011;		
Best Local Similarity 98.4%; Pred. No. 5.2e-76;		
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;		
Qy	1	MSTNPKQKKNKNTNRRPDQVFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
Db	1	MSTNPKQKKNKNTNRRPDQVFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
Qy	61	RRQPIPKARRPEGRTWAOQGYPMPLYGNECGWAGLLSPRGSRPSWGPTDPRRRSRNLG 120
Db	61	RRQPIPKARRPEGRTWAOQGYPMPLYGNECGWAGLLSPRGSRPSWGPTDPRRRSRNLG 120
Qy	121	KVIDTLTCGFADLMGYIPAVGAPLGGNARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
Db	121	KVIDTLTCGFADLMGYIPLVGAPLGGNARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
Qy	181	LLSCLTVPASA 191
Db	181	LLSCLTVPASA 191

RESULT 3		
GNWVCJ		
genome polyprotein - hepatitis C virus (strain J)		
N;Contains: capsid protein C; envelope protein M; major envelope protein E; nonstructural		
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5		
C;Species: hepatitis C virus		
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004		
A;Accession: A39253; PS0086		
R;Kato, N.; Hijikata, M.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Sugimura, T.; Shimoto		
Proc. Natl. Acad. Sci. U.S.A. 87, 9524-9528, 1990		
A;Title: Molecular cloning of the human hepatitis C virus genome from Japanese patients v		
A;Reference number: A39253; MUID:91088550; PMID:2175903		
A;Accession: A39253		
A;Molecule type: genomic RNA		
A;Residues: 1-3010 <KAT>		
A;Cross-references: UNIPROT:P26662; GB:D90208; NID:G221610; PIDN:BA414233.1; PID:G221611		
R;Kato, N.; Ohkoshi, S.; Shimotohno, K.		
Proc. Jpn. Acad. 65B, 219-223, 1989		
A;Title: Japanese isolates of the non-A, non-B hepatitis viral genome show sequence vari		
A;Reference number: PS0085		
A;Accession: PS0086		
A;Molecule type: genomic RNA		
A;Residues: 2650-2707 <KA2>		
A;Experimental source: Japanese isolate		
A;Comment: The cleavage sites of this polyprotein have not been determined.		
C;Superfamily: hepatitis C virus genome polyprotein		
C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serine		
F;2-115/Product: capsid protein C #status predicted <CPC>		
F;116-191/Product: envelope protein M #status predicted <EPM>		
F;192-389/Product: major envelope protein E #status predicted <MEE>		
F;390-729/Product: nonstructural protein NS1 #status predicted <NS1>		
F;730-1006/Product: nonstructural protein NS2 #status predicted <NS2>		
F;1007-1615/Product: hepatitis virus #status predicted <NS3>		
F;1230-1237/Region: nucleotide-binding motif A (P-loop)		
F;1312-1317/Region: nucleotide-binding motif B		
F;1316-1319/Region: DEXH motif		
F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4a>		
F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4b>		
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>		
F;196,209,234,250,305,325,417,423,430,448,532,556,576,623,645,1213,1255,2041,2077,2240,21		
Query Match 97.6%; Score 1015; DB 1; Length 3010;		
Best Local Similarity 97.4%; Pred. No. 4.2e-75;		
Matches 186; Conservative 2; Mismatches 3; Indels 0; Gaps 0;		
Qy	1	MSTNPKQKKNKNTNRRPDQVFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
Db	1	MSTNPKQKKNKNTNRRPDQVFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
Qy	61	RRQPIPKARRPEGRTWAOQGYPMPLYGNECGWAGLLSPRGSRPSWGPTDPRRRSRNLG 120
Db	61	RRQPIPKARRPEGRTWAOQGYPMPLYGNECGWAGLLSPRGSRPSWGPTDPRRRSRNLG 120
Qy	121	KVIDTLTCGFADLMGYIPAVGAPLGGNARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
Db	121	KVIDTLTCGFADLMGYIPLVGAPLGGNARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
Qy	181	LLSCLTVPASA 191
Db	181	LLSCLTVPASA 191
RESULT 4		
S40770		
genome polyprotein - hepatitis C virus		
N;Contains: capsid protein C; envelope protein M; hepatitis virus (EC 3.4.21.98) (nonstructu		
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5		
C;Species: hepatitis C virus		
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004		
A;Accession: S40770; PC1285		
R;Okamoto, H.		

submitted to the EMBL Data Library, March 1992

A;Reference number: S40770
A;Accession: S40770
A;Molecule type: genomic RNA
A;Residues: 1-3011 <OKA>
A;Cross-references: UNIPROT:Q03463; EMBL:D10749; NID:g221586; PIDN:BAA01582.1; PID:g221586
R;Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Yoshizawa, H.; Tsuda, Jpn. J. Exp. Med. 60, 167-177, 1990

A;Title: The 5'-terminal sequence of the hepatitis C virus genome.

A;Reference number: FCI284; MUID:9103116; PMID:2170712

A;Accession: FCI285

A;Molecule type: genomic RNA

A;Residues: 1-513 <OK2>

A;Cross-references: GB:D00831; NID:g221511; PIDN:BAA00705.1; PID:g221512

A;Experimental source: isolate HC-J1

C;Superfamily: hepatitis C virus genome polyprotein

C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin

F;2-115/Product: capsid protein C #status predicted <CPC>

F;116-191/Product: envelope protein M #status predicted <EPM>

F;192-389/Product: major envelope protein E #status predicted <MEE>

F;390-729/Product: nonstructural protein NS1 #status predicted <NS1>

F;730-1006/Product: nonstructural protein NS2 #status predicted <NS2>

F;1007-1615/Product: hepatitis C virus genome polyprotein

F;1230-1237/Region: nucleotide-binding motif A (P-loop)

F;1312-1317/Region: nucleotide-binding motif B

F;1316-1319/Region: DEXH motif

F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>

F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>

F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>

Query Match 97.4%; Score 1013; DB 1; Length 3011;
Best Local Similarity 97.4%; Pred. No. 6.1e-75;
Matches 186; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNKNTNRPPQDVKFPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

Db 1 MSTIPKQKNTNRPPQDVKFPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

Qy 61 RRQPIKARRPEGRTPWAPGYPMWLYGNECGWAGWLLSPRSPSPSGPTDPRRSNGLG 120

Db 61 RRQPIKARRPEGRTPWAPGYPMWLYGNECGWAGWLLSPRSPSPSGPTDPRRSNGLG 120

Qy 121 KVDTLTGCFADLMGYIPVAGCAPLGGAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180

Db 121 KVDTLTGCFADLMGYIPVAGCAPLGGAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191

Db 181 LLSCLTVPASA 191

RESULT 5

JQ1584

genome polyprotein - hepatitis C virus (strain U.K.) (fragment)

N;Contains: core protein C; envelope protein E1; envelope protein E2; nonstructural prot

C;Species: hepatitis C virus

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C;Accession: JQ1584

R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.

J. Gen. Virol. 73, 1521-1525, 1992

A;Title: Cloning and sequencing of the structural region and expression of putative core

A;Reference number: JQ1584; MUID:92300349; PMID:1318944

A;Accession: JQ1584

A;Molecule type: genomic RNA

A;Residues: 1-640 <KUM>

A;Cross-references: UNIPROT:Q68966; GB:X84079; NID:g643119; PIDN:CAA58888.1; PID:g643120

C;Superfamily: hepatitis C virus genome polyprotein

C;Keywords: core protein; envelope protein; glycoprotein; nonstructural protein; polypro

F;1-191/Product: core protein C #status predicted <CPC>

F;192-389/Product: envelope protein E1 #status predicted <EE1>

F;390-640/Product: envelope protein E2 and nonstructural protein NS1 #status predicted <

F;196, 209, 234, 305, 417, 430, 448, 476, 540, 556, 576, 623/Binding site: carbohydrate (Asn) (cova

Query Match 97.2%; Score 1011; DB 2; Length 640;
Best Local Similarity 96.9%; Pred. No. 2.1e-75;
Matches 185; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNKNTNRPPQDVKFPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

Db 1 MSTNPKQKNTNRPPQDVKFPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

Qy 61 RRQPIKARRPEGRTPWAPGYPMWLYGNECGWAGWLLSPRSPSPSGPTDPRRSNGLG 120

Db 61 RRQPIKARRPEGRTPWAPGYPMWLYGNECGWAGWLLSPRSPSPSGPTDPRRSNGLG 120

Qy 121 KVDTLTGCFADLMGYIPVAGCAPLGGAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180

Db 121 KVDTLTGCFADLMGYIPVAGCAPLGGAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191

Db 181 LLSCLTVPASA 191

RESULT 6

S12707

genome polyprotein - hepatitis C virus (fragment)

N;Contains: core protein; envelope protein

C;Species: hepatitis C virus

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: S12707

R;Takeuchi, K.; Kubo, Y.; Boonmar, S.; Watanabe, Y.; Katayama, T.; Choo, Q.-L.; Kuo, G.;

Nucleic Acids Res. 18, 4626, 1990

A;Title: Nucleotide sequence of core and envelope genes of the hepatitis C virus genome

A;Reference number: S12707; MUID:90356432; PMID:2117749

A;Accession: S12707

A;Molecule type: genomic RNA

A;Residues: 1-441 <TAK>

A;Cross-references: UNIPROT:Q81776; EMBL:D00574; NID:g221656; PIDN:BAA00452.1; PID:g221656

C;Superfamily: hepatitis C virus genome polyprotein

C;Keywords: polyprotein

Query Match 97.1%; Score 1010; DB 2; Length 441;
Best Local Similarity 96.9%; Pred. No. 1.8e-75;
Matches 185; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNKNTNRPPQDVKFPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

Db 1 MSTNPKQKNTNRPPQDVKFPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

Qy 61 RRQPIKARRPEGRTPWAPGYPMWLYGNECGWAGWLLSPRSPSPSGPTDPRRSNGLG 120

Db 61 RRQPIKARRPEGRTPWAPGYPMWLYGNECGWAGWLLSPRSPSPSGPTDPRRSNGLG 120

Qy 121 KVDTLTGCFADLMGYIPVAGCAPLGGAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180

Db 121 KVDTLTGCFADLMGYIPVAGCAPLGGAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191

Db 181 LLSCLTVPASA 191

RESULT 7

S32740

polyprotein - hepatitis C virus (isolate Russian) (fragment)

N;Contains: capsid protein C; envelope protein M

C;Species: hepatitis C virus

C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004

C;Accession: S32740

R;Vassiliev, V.B.; Viazov, S.O.; Kotova, E.Y.; Nosikov, V.V.

submitted to the EMBL Data Library, April 1993

A;Description: Evidence of new HCV variant of European isolate in Russia.

A;Reference number: S32740

A;Accession: S32740

A;Molecule type: genomic RNA

A;Residues: 1-189 <VAS>
A;Cross-references: UNIPROT:Q68873; EMBL:X71407
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein; envelope protein; polyprotein
F;1-115/Product: capsid protein C #status predicted <CPC>
F;116-189/Product: envelope protein M #status predicted <EPM>

Query Match 97.0%; Score 1009; DB 2; Length 189;
Best Local Similarity 97.9%; Pred. No. 9.7e-76;
Matches 185; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSTNPKPKQKKNNTNRRPDQVFPGGQIVGGVYLLPRRGLGVRATKTSERSQPRG 60
DB 1 MSTNPKPQRTKNTNRRPDQVFPGGQIVGGVYLLPRRGLGVRATKTSERSQPRG 60

QY 61 RRQPIPKARPEGRTPWAQPGYPMPLVYNECGWAGLLSPRGRPSWGPTDPRRRSRNLG 120
DB 61 RRQPIPKARPEGRTPWAQPGYPMPLVYNECGWAGLLSPRGRPSWGPTDPRRRSRNLG 120

QY 121 KVDTLTTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVDTLTTCGFADLMGYIPVGLGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180

QY 181 LLSCLTVPA 189
DB 181 LLSCLTVPA 189

RESULT 8
S18031
genome polyprotein - hepatitis C virus (isolate JK2) (fragment)
N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C;Species: hepatitis C virus
A;Variety: isolate JK2
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S18031
R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus iso
A;Reference number: S18029
A;Accession: S18031
A;Molecule type: Genomic RNA
A;Residues: 1-782 <HON>
A;Cross-references: UNIPROT:Q68950; EMBL:X61593
A;Experimental source: isolate JK2
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
F;1-191/Product: core protein #status predicted <MAT1>
F;192-383/Product: envelope protein 1 #status predicted <MAT2>
F;384-733/Product: NS1/E2 protein #status predicted <MAT3>
F;734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>

Query Match 96.7%; Score 1006; DB 2; Length 782;
Best Local Similarity 96.3%; Pred. No. 6.5e-75;
Matches 184; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSTNPKPKQKKNNTNRRPDQVFPGGQIVGGVYLLPRRGLGVRATKTSERSQPRG 60
DB 1 MSTNPKPQRTKNTNRRPDQVFPGGQIVGGVYLLPRRGLGVRATKTSERSQPRG 60

QY 61 RRQPIPKARPEGRTPWAQPGYPMPLVYNECGWAGLLSPRGRPSWGPTDPRRRSRNLG 120
DB 61 RRQPIPKARPEGRTPWAQPGYPMPLVYNECGWAGLLSPRGRPSWGPTDPRRRSRNLG 120

QY 121 KVDTLTTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVDTLTTCGFADLMGYIPVGLGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180

QY 181 LLSCLTVPA 191
DB 181 LLSCLTVPA 191

RESULT 9
PN0677
hypothetical protein 787 - hepatitis C virus (fragment)
C;Species: hepatitis C virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: PN0677
R;Cho, S.H.; Yoon, J.I.; Chang, J.E.; Ahn, B.M.; Lee, C.H.; Lee, Y.I.
Biochem. Biophys. Res. Commun. 196, 780-788, 1993
A;Title: Genomic typing of hepatitis C viruses from Korean patients: Implications of gen
A;Reference number: PN0677; MUID:94059104; PMID:8240354
A;Accession: PN0677
A;Molecule type: mRNA
A;Residues: 1-787 <CHO>
A;Cross-references: UNIPROT:Q08244; GB:120498; NID:gl381031; PIDN:AAB02608.1; PID:gl3810
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: glycoprotein; nonstructural protein
F;196,209,234,250,305,325,421,427,452,536,544,560,580,627,649/Binding site: carbohydrate

Query Match 96.7%; Score 1006; DB 2; Length 787;
Best Local Similarity 96.3%; Pred. No. 6.5e-75;
Matches 184; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSTNPKPKQKKNNTNRRPDQVFPGGQIVGGVYLLPRRGLGVRATKTSERSQPRG 60
DB 1 MSTNPKPQRTKNTNRRPDQVFPGGQIVGGVYLLPRRGLGVRATKTSERSQPRG 60

QY 61 RRQPIPKARPEGRTPWAQPGYPMPLVYNECGWAGLLSPRGRPSWGPTDPRRRSRNLG 120
DB 61 RRQPIPKARPEGRTPWAQPGYPMPLVYNECGWAGLLSPRGRPSWGPTDPRRRSRNLG 120

QY 121 KVDTLTTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVDTLTTCGFADLMGYIPVGLGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180

QY 181 LLSCLTVPA 191
DB 181 LLSCLTVPA 191

RESULT 10
GNWVTC
genome polyprotein - hepatitis C virus
N;Contains: capsid protein C; envelope protein M; hepatitis protein NS5 (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: A38465
R;Takamizawa, A.; Mori, C.; Fuke, I.; Manabe, S.; Murakami, S.; Fujita, J.; Onishi, E.;
J. Virol. 65, 1105-1113, 1991
A;Title: Structure and organization of the hepatitis C virus genome isolated from human
A;Reference number: A38465; MUID:91140698; PMID:1847440
A;Accession: A38465
A;Molecule type: Genomic RNA
A;Residues: 1-3010 <TAK>
A;Cross-references: UNIPROT:P26663; EMBL:M58335; NID:g329770; PIDN:AAA72945.1; PID:g3297;
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructural
F;2-115/Product: capsid protein C #status predicted <CPC>
F;116-191/Product: envelope protein M #status predicted <EPM>
F;192-389/Product: major envelope protein NS1 #status predicted <NS1>
F;390-729/Product: nonstructural protein NS2 #status predicted <NS2>
F;730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F;1007-1615/Product: hepatitis protein #status predicted <NS3>
F;1230-1237/Region: nucleotide-binding motif A (P-loop)
F;1312-1317/Region: nucleotide-binding motif B
F;1316-1319/Region: DEXH motif
F;1863-2013/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,2077,224

Query Match 96.7%; Score 1006; DB 1; Length 3010;
Best Local Similarity 96.9%; Pred. No. 2.3e-74;

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RESULT 14
A44150
structural protein - hepatitis C virus
C;Species: hepatitis C virus
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A44150
R;Ching, W.M.; Wychowiski, C.; Beach, M.J.; Wang, H.; Davies, C.L.; Carl, M.; Bradley, D.

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OM protein - protein search, using sw model

Run on: August 19, 2005, 12:43:21 ; Search time 107 Seconds
(without alignments)

698.999 Million cell updates/sec

Title: US-10-770-117-2

Perfect score: 1040

Sequence: 1 MSTNPKQKKNKNTNRPPQ.....CSPSIFLLALLSLCTVPASA 191

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1040	100.0	191	18	US-10-770-117-2
2	1035	99.5	191	18	US-10-770-117-4
3	1035	99.5	3011	9	US-09-916-359-2
4	1035	99.5	3011	16	US-10-445-724-2
5	1031	99.1	190	14	US-10-268-562-1
6	1030	99.0	190	15	US-10-450-649-7
7	1026	98.7	249	15	US-10-365-620-54
8	1026	98.7	249	17	US-10-912-969-56
9	1026	98.7	450	15	US-10-651-165-179
10	1026	98.7	450	15	US-10-651-165-180
11	1026	98.7	473	15	US-10-365-620-56

12	1026	98.7	473	17	US-10-912-969-58
13	1026	98.7	473	17	US-10-913-171-39
14	1026	98.7	3011	9	US-09-742-659-4
15	1026	98.7	3011	9	US-09-952-572-9
16	1026	98.7	3011	9	US-09-929-955-1
17	1026	98.7	3011	9	US-09-747-419-20
18	1026	98.7	3011	10	US-09-891-894-3
19	1026	98.7	3011	13	US-10-104-966-1
20	1026	98.7	3011	14	US-10-259-275-20
21	1026	98.7	3011	14	US-10-184-150-3
22	1026	98.7	3011	15	US-10-328-997-3
23	1026	98.7	3011	15	US-10-189-359-14
24	1026	98.7	3011	15	US-10-296-734-406
25	1026	98.7	3011	15	US-10-719-619-1
26	1026	98.7	3011	15	US-10-817-591-1
27	1026	98.7	3011	20	US-11-006-313-20
28	1026	98.7	3012	9	US-09-238-076-2
29	1026	98.7	3012	10	US-09-995-937-2
30	1026	98.7	3012	10	US-09-917-563-2
31	1022	98.3	3011	9	US-09-238-076-20
32	1022	98.3	3011	10	US-09-995-937-20
33	1022	98.3	3011	10	US-09-917-563-20
34	1015	97.6	450	15	US-10-651-165-187
35	1013	97.4	450	15	US-10-651-165-181
36	1013	97.4	2894	9	US-09-941-611-23
37	1013	97.4	2894	14	US-10-044-995-23
38	1013	97.4	2894	17	US-10-823-871-23
39	1011	97.2	450	15	US-10-651-165-190
40	1011	97.2	3011	14	US-10-232-643-6
41	1007	96.8	809	9	US-09-973-025-50
42	1007	96.8	809	10	US-09-899-303-50
43	1007	96.8	809	10	US-09-995-808-50
44	1007	96.8	809	10	US-09-995-860-50
45	1007	96.8	809	10	US-09-995-791-50

ALIGNMENTS

RESULT 1

US-10-770-117-2
; Sequence 2, Application US/10770117
; Publication No. US20050129705A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States, as represented by the
; APPLICANT: Secretary, Dept. of
; APPLICANT: Health and Human Services
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Sarobe, Pablo
; APPLICANT: Pendleton, C. David
; APPLICANT: Reinstone, Stephen M.
; APPLICANT: Arichi, Tatsumi
; APPLICANT: Major, Marian E.
; TITLE OF INVENTION: MODIFIED HCV PEPTIDE VACCINES
; FILE REFERENCE: 14014.0347/P
; CURRENT APPLICATION NUMBER: US/10/770,117
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: US/09/763,260
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/097,446
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: synthetic construct
US-10-770-117-2

Query Match 100.0%; Score 1040; DB 18; Length 191;

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Best Local Similarity 100.0%; Pred. No. 5.2e-80;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60

QY 61 RRQIPKARPEGRTWAQPGYPWPLYGNECGWAGWLLSPGSRPSWGPTDPRRSRNLG 120
Db 61 RRQIPKARPEGRTWAQPGYPWPLYGNECGWAGWLLSPGSRPSWGPTDPRRSRNLG 120

QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180

QY 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 2
US-10-770-117-4
; Sequence 4, Application US/10770117
; Publication No. US20050129705A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States, as represented by the
; APPLICANT: Secretary, Dept. of
; APPLICANT: Health and Human Services
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Sarobe, Pablo
; APPLICANT: Pendleton, C. David
; APPLICANT: Feinstein, Stephen M.
; APPLICANT: Arichi, Tatsuaki
; APPLICANT: Major, Marian E.
; TITLE OF INVENTION: MODIFIED HCV PEPTIDE VACCINES
; FILE REFERENCE: 14014.0347/P
; CURRENT APPLICATION NUMBER: US/10/770,117
; CURRENT FILING DATE: 2004-02-02
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US/09/763,260
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/097,446
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: synthetic construct
US-10-770-117-4

Query Match 99.5%; Score 1035; DB 18; Length 191;
Best Local Similarity 99.5%; Pred. No. 1.4e-79;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60

QY 61 RRQIPKARPEGRTWAQPGYPWPLYGNECGWAGWLLSPGSRPSWGPTDPRRSRNLG 120
Db 61 RRQIPKARPEGRTWAQPGYPWPLYGNECGWAGWLLSPGSRPSWGPTDPRRSRNLG 120

QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180

QY 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191
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RESULT 3
US-09-916-359-2
; Sequence 2, Application US/09916359
; Patent No. US20020034734A1
; GENERAL INFORMATION:
; APPLICANT: Veronique Barban
; TITLE OF INVENTION: VACCINE COMPOSITION FOR PREVENTING OR
; TITLE OF INVENTION: TREATING C HEPATITIS
; FILE REFERENCE: PMCF97-03A
; CURRENT APPLICATION NUMBER: US/09/916,359
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 09/388,874
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 97/02,887
; PRIOR FILING DATE: 1997-03-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3011
; TYPE: PRT
; ORGANISM: Virus
US-09-916-359-2

Query Match 99.5%; Score 1035; DB 9; Length 3011;
Best Local Similarity 99.5%; Pred. No. 2.5e-78;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60

QY 61 RRQIPKARPEGRTWAQPGYPWPLYGNECGWAGWLLSPGSRPSWGPTDPRRSRNLG 120
Db 61 RRQIPKARPEGRTWAQPGYPWPLYGNECGWAGWLLSPGSRPSWGPTDPRRSRNLG 120

QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180

QY 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 4
US-10-445-724-2
; Sequence 2, Application US/10445724
; Publication No. US20040101829A1
; GENERAL INFORMATION:
; APPLICANT: STAPLETON, JACK T.
; APPLICANT: WUENSCHMANN, SABINA
; TITLE OF INVENTION: A PROTEIN THAT INTERACTS WITH LIPIDS AND
; TITLE OF INVENTION: METHODS FOR TREATING HYPERLIPIDEMIA
; FILE REFERENCE: IOWA:045US
; CURRENT APPLICATION NUMBER: US/10/445,724
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: 60/392,158
; PRIOR FILING DATE: 2003-05-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3011
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-445-724-2

Query Match 99.5%; Score 1035; DB 16; Length 3011;
Best Local Similarity 99.5%; Pred. No. 2.5e-78;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
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Db      1 MSTNPKQKKNKNTNRRPQDVKPPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
Qy      61 RROPIPKARPEGRWTWAPGYWPLYNCGCGWAGWLLSPRGSRPSWGPTDPRRSRNLG 120
Db      61 RROPIPKARPEGRWTWAPGYWPLYNCGCGWAGWLLSPRGSRPSWGPTDPRRSRNLG 120
Qy      121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
Db      121 KVIDTLTCGFADLMGYIPVAGAPLGGAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
Qy      181 LLSCLTVPASA 191
Db      181 LLSCLTVPASA 191

RESULT 5
US-10-268-562-1
; Sequence 1, Application US/10268562
; Publication No. US20030108563A1
; GENERAL INFORMATION:
; APPLICANT: Otho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: Reagents for the simultaneous detection of HCV core antigens and
; FILE REFERENCE: antibodies
; CURRENT APPLICATION NUMBER: US/10/268,562
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/347,943
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-268-562-1

Query Match      99.1%; Score 1031; DB 14; Length 190;
Best Local Similarity 99.5%; Pred. No. 3e-79;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MSTNPKQKKNKNTNRRPQDVKPPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
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Qy      61 RROPIPKARPEGRWTWAPGYWPLYNCGCGWAGWLLSPRGSRPSWGPTDPRRSRNLG 120
Db      61 RROPIPKARPEGRWTWAPGYWPLYNCGCGWAGWLLSPRGSRPSWGPTDPRRSRNLG 120
Qy      121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
Db      121 KVIDTLTCGFADLMGYIPVAGAPLGGAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
Qy      181 LLSCLTVPAS 190
Db      181 LLSCLTVPAS 190

RESULT 6
US-10-450-649-7
; Sequence 7, Application US/10450649
; Publication No. US20040052818A1
; GENERAL INFORMATION:
; APPLICANT: Heinz, Franz X.
; TITLE OF INVENTION: ATTENUATED LIVE VACCINE
; FILE REFERENCE: U 014666-0
; CURRENT APPLICATION NUMBER: US/10/450,649
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/AT02/00046
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: A 272/2001 AT
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 9
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Hepatitis C Virus 1
US-10-450-649-7

Query Match      99.0%; Score 1030; DB 15; Length 190;
Best Local Similarity 99.5%; Pred. No. 3.6e-79;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 STNPKQKKNKNTNRRPQDVKPPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 61
Db      1 STNPKQKKNKNTNRRPQDVKPPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
Qy      62 RROPIPKARPEGRWTWAPGYWPLYNCGCGWAGWLLSPRGSRPSWGPTDPRRSRNLG 121
Db      61 RROPIPKARPEGRWTWAPGYWPLYNCGCGWAGWLLSPRGSRPSWGPTDPRRSRNLG 120
Qy      122 VIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 181
Db      121 VIDTLTCGFADLMGYIPVAGAPLGGAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
Qy      182 LLSCLTVPASA 191
Db      181 LLSCLTVPASA 190

RESULT 7
US-10-365-620-54
; Sequence 54, Application US/10365620
; Publication No. US20040001853A1
; GENERAL INFORMATION:
; APPLICANT: George, Rajan
; APPLICANT: Tyrrell, Lorne
; TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response
; FILE REFERENCE: 656.0016
; CURRENT APPLICATION NUMBER: US/10/365,620
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US60/423,578
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: 60/390,564
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 249
; TYPE: PRT
; ORGANISM: ORF of HCV Core Protein
US-10-365-620-54

Query Match      98.7%; Score 1026; DB 15; Length 249;
Best Local Similarity 98.4%; Pred. No. 1e-78;
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 MSTNPKQKKNKNTNRRPQDVKPPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
Db      31 MSTNPKQKKNTNRRPQDVKPPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 90
Qy      61 RROPIPKARPEGRWTWAPGYWPLYNCGCGWAGWLLSPRGSRPSWGPTDPRRSRNLG 120
Db      91 RROPIPKARPEGRWTWAPGYWPLYNCGCGWAGWLLSPRGSRPSWGPTDPRRSRNLG 150
Qy      121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
Db      151 KVIDTLTCGFADLMGYIPVAGAPLGGAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 210
Qy      181 LLSCLTVPASA 191
Db      211 LLSCLTVPASA 221
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RESULT 8
US-10-912-969-56
; Sequence 56, Application US/10912969
; Publication No. US20050013828A1
; GENERAL INFORMATION:
; APPLICANT: Virexx Research, Inc.
; APPLICANT: George, Rajan
; APPLICANT: Tyrrell, Lorne
; APPLICANT: Noujaim, Antoine
; APPLICANT: Wang, Dakun
; APPLICANT: Ma, Allan
; TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response
; FILE REFERENCE: 17506-007001
; CURRENT APPLICATION NUMBER: US/10/912,969
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: US 60/390,564
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 60/423,578
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 10/365,620
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: PCT/IB04/00373
; PRIOR FILING DATE: 2004-02-14
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-912-969-56

Query Match          98.7%; Score 1026; DB 17; Length 249;
Best Local Similarity 98.4%; Pred. No. 1e-78; 2; Indels 0; Gaps 0;
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSTNPKPKQKKKNTNRRPQDVKFPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60
Db 31 MSTNPKPQKTKNTNRRPQDVKFPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 90
QY 61 RRQIPKARRPEGRRTWAQPGYWPPLYGNECCGAGWLLSPRGRPSWGPTDPRRRRNIG 120
Db 91 RRQIPKARRPEGRRTWAQPGYWPPLYGNECCGAGWLLSPRGRPSWGPTDPRRRRNIG 150
QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
Db 151 KVIDTLTCGFADLMGYIPVVGAPLGGAAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 210
QY 181 LLSCLTVPASA 191
Db 211 LLSCLTVPASA 221

RESULT 9
US-10-651-165-179
; Sequence 179, Application US/10651165
; Publication No. US20040047877A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 179
; LENGTH: 450
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-179

Query Match          98.7%; Score 1026; DB 15; Length 450;
Best Local Similarity 98.4%; Pred. No. 2e-78; 2; Indels 0; Gaps 0;
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSTNPKPKQKKKNTNRRPQDVKFPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60
Db 1 MSTNPKPQKTKNTNRRPQDVKFPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60
QY 61 RRQIPKARRPEGRRTWAQPGYWPPLYGNECCGAGWLLSPRGRPSWGPTDPRRRRNIG 120
Db 61 RRQIPKARRPEGRRTWAQPGYWPPLYGNECCGAGWLLSPRGRPSWGPTDPRRRRNIG 120
QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPVVGAPLGGAAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 10
US-10-651-165-180
; Sequence 180, Application US/10651165
; Publication No. US20040047877A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 180
; LENGTH: 450
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-180

Query Match          98.7%; Score 1026; DB 15; Length 450;
Best Local Similarity 98.4%; Pred. No. 2e-78; 2; Indels 0; Gaps 0;
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSTNPKPKQKKKNTNRRPQDVKFPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60
Db 1 MSTNPKPQKTKNTNRRPQDVKFPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60
QY 61 RRQIPKARRPEGRRTWAQPGYWPPLYGNECCGAGWLLSPRGRPSWGPTDPRRRRNIG 120
Db 61 RRQIPKARRPEGRRTWAQPGYWPPLYGNECCGAGWLLSPRGRPSWGPTDPRRRRNIG 120
QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPVVGAPLGGAAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191
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RESULT 11
US-10-365-620-56
; Sequence 56, Application US/10365620
; Publication No. US20040001853A1
; GENERAL INFORMATION:
; APPLICANT: George, Rajan
; APPLICANT: Tyrell, Lorne
; APPLICANT: Tyrrell, Lorne
; TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response
; FILE REFERENCE: 656.0016
; CURRENT APPLICATION NUMBER: US/10/365,620
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US60/423,578
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: 60/390,564
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 473
; TYPE: PRT
; ORGANISM: ORF of HCV Core-TBD protein
US-10-365-620-56

Query Match          98.7%; Score 1026; DB 15; Length 473;
Best Local Similarity 98.4%; Pred. No. 2.1e-78;
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSTNPKPKKKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 60
Db 31 MSTNPKPKQTKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 90
Qy 61 RRQPIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGSRRPSWGPTDPRRRSRNLG 120
Db 91 RRQPIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGSRRPSWGPTDPRRRSRNLG 150
Qy 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db 151 KVIDTLTCGFADLMGYIPVGVAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 210
Qy 181 LLSCLTVPASA 191
Db 211 LLSCLTVPASA 221

RESULT 12
US-10-912-969-58
; Sequence 58, Application US/10912969
; Publication No. US20050013828A1
; GENERAL INFORMATION:
; APPLICANT: Virexx Research, Inc.
; APPLICANT: George, Rajan
; APPLICANT: Tyrell, Lorne
; APPLICANT: Noujaim, Antoine
; APPLICANT: Wang, Dakun
; APPLICANT: Ma, Allan
; TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response
; FILE REFERENCE: 17506-007001
; CURRENT APPLICATION NUMBER: US/10/912,969
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: US 60/390,564
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 60/423,578
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 10/365,620
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: PCT/IB04/00373
; PRIOR FILING DATE: 2004-02-14
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
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; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-912-969-58

Query Match          98.7%; Score 1026; DB 17; Length 473;
Best Local Similarity 98.4%; Pred. No. 2.1e-78;
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSTNPKPKKKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 60
Db 31 MSTNPKPKQTKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 90
Qy 61 RRQPIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGSRRPSWGPTDPRRRSRNLG 120
Db 91 RRQPIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGSRRPSWGPTDPRRRSRNLG 150
Qy 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db 151 KVIDTLTCGFADLMGYIPVGVAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 210
Qy 181 LLSCLTVPASA 191
Db 211 LLSCLTVPASA 221

RESULT 13
US-10-913-171-39
; Sequence 39, Application US/10913171
; Publication No. US20050031628A1
; GENERAL INFORMATION:
; APPLICANT: Virexx Research, Inc.
; APPLICANT: George, Rajan
; APPLICANT: Tyrrell, Lorne
; APPLICANT: Noujaim, Antoine
; APPLICANT: Wang, Dakun
; APPLICANT: Ma, Allan
; TITLE OF INVENTION: CHIMERIC ANTIGENS FOR BREAKING HOST TOLERANCE TO FOREIGN ANTIGENS
; FILE REFERENCE: 17506-006001
; CURRENT APPLICATION NUMBER: US/10/913,171
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: US 60/493,449
; PRIOR FILING DATE: 2004-08-08
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-913-171-39

Query Match          98.7%; Score 1026; DB 17; Length 473;
Best Local Similarity 98.4%; Pred. No. 2.1e-78;
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSTNPKPKKKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 60
Db 31 MSTNPKPKQTKNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 90
Qy 61 RRQPIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGSRRPSWGPTDPRRRSRNLG 120
Db 91 RRQPIPKARRPEGRRTWAQPGYPWPLYGNECGWAGWLLSPRGSRRPSWGPTDPRRRSRNLG 150
Qy 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
Db 151 KVIDTLTCGFADLMGYIPVGVAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 210
Qy 181 LLSCLTVPASA 191
Db 211 LLSCLTVPASA 221
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Db          211 LLSCLTVPASA 221

RESULT 14
US-09-742-659-4
; Sequence 4, Application US/09742659
; Patent No. US20010034019A1
; GENERAL INFORMATION:
; APPLICANT: Hong, Zhi
; APPLICANT: Butkiewicz, Nancy J.
; APPLICANT: Zhong, Weidong
; APPLICANT: Ingravallo, Paul
; APPLICANT: Wright-Minogue, Jacquelyn
; APPLICANT: Lau, Johnson Y.
; APPLICANT: Lemon, Stanley M.
; TITLE OF INVENTION: Chimeric HCV/GBV-B viruses
; FILE REFERENCE: ID01116
; CURRENT APPLICATION NUMBER: US/09/742,659
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 60/171,469
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 3011
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; US-09-742-659-4

Query Match          98.7%; Score 1026; DB 9; Length 3011;
Best Local Similarity 98.4%; Pred. No. 1.4e-77;
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 MSTNPKPQKNKNTNRRPDVKFPGGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 60
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Db      1 MSTNPKPQKTKNTNRRPDVKFPGGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      61 RRQPIPKARRPEGRTPAQGPWPPLYGNECGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 RRQPIPKARRPEGRTPAQGPWPPLYGNECGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      121 KVIDLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      121 KVIDLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      181 LLSCLTVPASA 191
        |||||:|||||
Db      181 LLSCLTVPASA 191
        |||||:|||||

Search completed: August 19, 2005, 13:01:50
Job time : 108 secs

Query Match          98.7%; Score 1026; DB 9; Length 3011;
Best Local Similarity 98.4%; Pred. No. 1.4e-77;
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 MSTNPKPQKNKNTNRRPDVKFPGGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MSTNPKPQKTKNTNRRPDVKFPGGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      61 RRQPIPKARRPEGRTPAQGPWPPLYGNECGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 RRQPIPKARRPEGRTPAQGPWPPLYGNECGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      121 KVIDLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      121 KVIDLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      181 LLSCLTVPASA 191
        |||||:|||||
Db      181 LLSCLTVPASA 191
        |||||:|||||

RESULT 15
US-09-952-572-9
; Sequence 9, Application US/09952572
; Patent No. US20020119495A1
; GENERAL INFORMATION:
; APPLICANT: HAWAII BIOTECHNOLOGY GROUP, Inc.
; APPLICANT: NAKANO, Eileen
; APPLICANT: CLEMENTS, David
; APPLICANT: HUMPHREYS, Tom
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITION OF HEPATITIS C
; FILE REFERENCE: HAWBIO1100
; CURRENT APPLICATION NUMBER: US/09/952,572
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: US 60/230,927
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 3011
; TYPE: PRT
; ORGANISM: Hepatitis C Virus
; US-09-952-572-9
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 19, 2005, 12:34:55 ; Search time 20 Seconds
(without alignments)
712.899 Million cell updates/sec

Title: US-10-770-117-2

Perfect score: 1040

Sequence: 1 MSTNPKQKKNKNTNRPO.....CSPSIFLLALLSCLTVPASA 191

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1040	100.0	191	4	US-09-763-260-2
2	1035	99.5	191	4	US-09-763-260-4
3	1035	99.5	3011	1	US-08-440-103-36
4	1035	99.5	3011	1	US-08-440-542-36
5	1035	99.5	3011	1	US-07-910-760-10
6	1035	99.5	3011	1	US-08-440-519-10
7	1035	99.5	3011	1	US-08-231-368-36
8	1035	99.5	3011	1	US-08-440-210-36
9	1035	99.5	3011	3	US-09-388-874-2
10	1035	99.5	3011	3	US-09-046-604-36
11	1035	99.5	3011	3	US-08-440-549-10
12	1035	99.5	3011	3	US-08-850-328-1
13	1035	99.5	3011	4	US-09-916-359-2
14	1031	99.1	215	1	US-07-681-703B-12
15	1031	99.1	215	1	US-07-681-703B-14
16	1031	99.1	215	5	PCT-US91-02370-12
17	1031	99.1	215	5	PCT-US91-02370-14
18	1031	99.1	217	2	US-08-407-410B-12
19	1031	99.1	217	2	US-08-407-410B-14
20	1031	99.1	217	2	US-08-485-500-12
21	1031	99.1	217	2	US-08-485-500-14
22	1029	98.9	2995	3	US-08-444-818-138
23	1026	98.7	191	2	US-08-290-665A-156
24	1026	98.7	191	2	US-08-290-665A-157
25	1026	98.7	191	2	US-08-290-665A-158
26	1026	98.7	191	2	US-08-290-665A-159
27	1026	98.7	191	2	US-08-290-665A-160

28	1026	98.7	191	3	US-08-380-160-3	Sequence 3, Appli
29	1026	98.7	191	5	PCT-US95-10398-156	Sequence 156, App
30	1026	98.7	191	5	PCT-US95-10398-157	Sequence 157, App
31	1026	98.7	191	5	PCT-US95-10398-158	Sequence 158, App
32	1026	98.7	191	5	PCT-US95-10398-159	Sequence 159, App
33	1026	98.7	191	5	PCT-US95-10398-160	Sequence 160, App
34	1026	98.7	450	4	US-08-635-886C-179	Sequence 179, App
35	1026	98.7	450	4	US-08-635-886C-180	Sequence 180, App
36	1026	98.7	450	4	US-08-974-690C-179	Sequence 179, App
37	1026	98.7	450	4	US-08-974-690C-180	Sequence 180, App
38	1026	98.7	967	1	US-08-188-281B-13	Sequence 13, Appl
39	1026	98.7	967	5	PCT-US94-07280-13	Sequence 13, Appl
40	1026	98.7	967	5	PCT-US95-01087-13	Sequence 13, Appl
41	1026	98.7	1648	1	US-08-188-281B-12	Sequence 12, Appl
42	1026	98.7	1648	5	PCT-US94-07280-12	Sequence 12, Appl
43	1026	98.7	1648	5	PCT-US95-01087-12	Sequence 12, Appl
44	1026	98.7	3011	1	US-08-188-281B-1	Sequence 1, Appli
45	1026	98.7	3011	1	US-08-453-552-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-763-260-2
; Sequence 2, Application US/09763260
; Patent No. 6685944
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States, as represented by the
; APPLICANT: Secretary, Dept. of
; APPLICANT: Health and Human Services
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Sarobe, Pablo
; APPLICANT: Pendleton, C. David
; APPLICANT: Feinstein, Stephen M.
; APPLICANT: Arichi, Tatsumi
; APPLICANT: Major, Marian E.
; TITLE OF INVENTION: MODIFIED HCV PEPTIDE VACCINES
; FILE REFERENCE: 14014.0347/P
; CURRENT APPLICATION NUMBER: US/09/763,260
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/097,446
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. 6685944e =
; OTHER INFORMATION: synthetic construct
US-09-763-260-2

Query Match	100.0%;	Score 1040;	DB 4;	Length 191;
Best Local Similarity	100.0%;	Pred. No. 1.3e-92;		
Matches 191;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	MSTNPKQKKNKNTNRPODVKPGGGQIVGGYLLPRGPRGLGVTRATKTSERSQPRG	60	
Db	1	MSTNPKQKKNKNTNRPODVKPGGGQIVGGYLLPRGPRGLGVTRATKTSERSQPRG	60	
Qy	61	RRQIPKARPEGRWQAQPGYPMPLVYNECGWAGLLSPRGRSPSGPTDPRRRSRNLG	120	
Db	61	RRQIPKARPEGRWQAQPGYPMPLVYNECGWAGLLSPRGRSPSGPTDPRRRSRNLG	120	
Qy	121	KVIDTLTCGFDLGMGYIPAVGAPLGGARALAHGVRVLEGVNVTATNLPCCGSPSIFLLA	180	
Db	121	KVIDTLTCGFDLGMGYIPAVGAPLGGARALAHGVRVLEGVNVTATNLPCCGSPSIFLLA	180	
Qy	181	LLSCLTVPASA	191	
Db	181	LLSCLTVPASA	191	

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RESULT 2
US-09-763-260-4
; Sequence 4, Application US/09763260
; Patent No. 6685944
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States, as represented by the
; APPLICANT: Secretary, Dept. of
; APPLICANT: Health and Human Services
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Sarobe, Pablo
; APPLICANT: Pendleton, C. David
; APPLICANT: Feinstein, Stephen M.
; APPLICANT: Arichi, Tatsumi
; APPLICANT: Major, Marian E.
; TITLE OF INVENTION: MODIFIED HCV PEPTIDE VACCINES
; FILE REFERENCE: 14014.0347/P
; CURRENT APPLICATION NUMBER: US/09/763,260
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/097,446
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. 6685944e =
; OTHER INFORMATION: synthetic construct
US-09-763-260-4

Query Match          99.5%; Score 1035; DB 4; Length 191;
Best Local Similarity 99.5%; Pred. No. 3.9e-92;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGRLGVRAATKTSERSQPRG 60
DB 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGRLGVRAATKTSERSQPRG 60
QY 61 RRQIPKARRPEGRWTAQGYPMPLVGNCGWAGWLLSPRGRSPSGWPTDPRRRSRNLG 120
DB 61 RRQIPKARRPEGRWTAQGYPMPLVGNCGWAGWLLSPRGRSPSGWPTDPRRRSRNLG 120
QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191

RESULT 3
US-08-440-103-36
; Sequence 36, Application US/08440103
; Patent No. 5670152
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/440,542
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,103
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3011 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-440-103-36

Query Match          99.5%; Score 1035; DB 1; Length 3011;
Best Local Similarity 99.5%; Pred. No. 1.1e-90;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGRLGVRAATKTSERSQPRG 60
DB 1 MSTNPKQKKNKNTNRRPDQVKFPGGGQIVGGVYLLPRGRLGVRAATKTSERSQPRG 60
QY 61 RRQIPKARRPEGRWTAQGYPMPLVGNCGWAGWLLSPRGRSPSGWPTDPRRRSRNLG 120
DB 61 RRQIPKARRPEGRWTAQGYPMPLVGNCGWAGWLLSPRGRSPSGWPTDPRRRSRNLG 120
QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191

RESULT 4
US-08-440-542-36
; Sequence 36, Application US/08440542
; Patent No. 5670153
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,542
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; COMPUTER: IBM PC compatible
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PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE: 07/1991
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3011 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-440-542-36

Query Match 99.5%; Score 1035; DB 1; Length 3011;
Best Local Similarity 99.5%; Pred. No. 1.1e-90;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNTNRRPQDVKPPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60
DB 1 MSTNPKQKKNTNRRPQDVKPPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

QY 61 RRQPIPKARRPEGRWTWQPGYWPPLYGNEGCGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120
DB 61 RRQPIPKARRPEGRWTWQPGYWPPLYGNEGCGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120

QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180

QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191

RESULT 5
US-07-910-760-10
; Sequence 10, Application US/07910760
; Patent No. 5683864
; GENERAL INFORMATION:
; APPLICANT: Houghton, Michael
; APPLICANT: Choo, Qui-Lim
; APPLICANT: Kuo, George
; TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: P.O. Box 8097 (Int. Prop. R-440)
; CITY: Emeryville
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/910,760
; FILING DATE: 07-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Blackburn Esq., Robert P.
; REGISTRATION NUMBER: 30,447
; REFERENCE/DOCKET NUMBER: 0101.002

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2702
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3011 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-910-760-10

Query Match 99.5%; Score 1035; DB 1; Length 3011;
Best Local Similarity 99.5%; Pred. No. 1.1e-90;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNTNRRPQDVKPPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60
DB 1 MSTNPKQKKNTNRRPQDVKPPGGQIVGGVYLLPRRGLGVRAATKTSERSQPRG 60

QY 61 RRQPIPKARRPEGRWTWQPGYWPPLYGNEGCGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120
DB 61 RRQPIPKARRPEGRWTWQPGYWPPLYGNEGCGWAGWLLSPRGRSPSWGPTDPRRRSRNLG 120

QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180

QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191

RESULT 6
US-08-440-519-10
; Sequence 10, Application US/08440519
; Patent No. 5712087
; GENERAL INFORMATION:
; APPLICANT: Houghton, Michael
; APPLICANT: Choo, Qui-Lim
; APPLICANT: Kuo, George
; TITLE OF INVENTION: Antigen for Use in Immunoassays for Anti-HCV Antibodies
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: P.O. Box 8097 (Int. Prop. R-440)
; CITY: Emeryville
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,519
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/910,760
; FILING DATE: 07-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Blackburn Esq., Robert P.
; REGISTRATION NUMBER: 30,447
; REFERENCE/DOCKET NUMBER: 0101.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2702
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3011 amino acids
; TYPE: amino acid

Db 61 RRQPIKARRPEGRWTAQPGYWPVLYNCGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
Qy 121 KVIDTLTCGFADLMGYIPAVGAPLGGAAALAHGVRVLEGVNATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPVGVGAPLGGAAALAHGVRVLEGVNATGNLPGCSFSIFLLA 180
Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 9

US-09-388-874-2
; Sequence 2, Application US/09388874
; Patent No. 6284249
; GENERAL INFORMATION:
; APPLICANT: Veronique Barban
; TITLE OF INVENTION: VACCINE COMPOSITION FOR PREVENTING OR
; FILE REFERENCE: PWC97-03A
; CURRENT APPLICATION NUMBER: US/09/388,874
; EARLIER FILING DATE: 1999-09-02
; EARLIER APPLICATION NUMBER: PCT/FR98/00448
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 97/02,887
; EARLIER FILING DATE: 1997-03-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3011
; TYPE: PRT
; ORGANISM: Virus
US-09-388-874-2

Query Match 99.5%; Score 1035; DB 3; Length 3011;
Best Local Similarity 99.5%; Pred. No. 1.1e-90;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MSTNPKQKKNKNTNRPPQDVKFGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKQKKNKNTNRPPQDVKFGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60
Qy 61 RRQPIKARRPEGRWTAQPGYWPVLYNCGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
Db 61 RRQPIKARRPEGRWTAQPGYWPVLYNCGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
Qy 121 KVIDTLTCGFADLMGYIPAVGAPLGGAAALAHGVRVLEGVNATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPVGVGAPLGGAAALAHGVRVLEGVNATGNLPGCSFSIFLLA 180
Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 10

US-09-046-604-36
; Sequence 36, Application US/09046604
; Patent No. 6303292
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
; CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 45
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,604
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3011 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-046-604-36

Query Match 99.5%; Score 1035; DB 3; Length 3011;
Best Local Similarity 99.5%; Pred. No. 1.1e-90;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MSTNPKQKKNKNTNRPPQDVKFGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKQKKNKNTNRPPQDVKFGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60
Qy 61 RRQPIKARRPEGRWTAQPGYWPVLYNCGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
Db 61 RRQPIKARRPEGRWTAQPGYWPVLYNCGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
Qy 121 KVIDTLTCGFADLMGYIPAVGAPLGGAAALAHGVRVLEGVNATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPVGVGAPLGGAAALAHGVRVLEGVNATGNLPGCSFSIFLLA 180
Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 11

US-08-440-549-10
; Sequence 10, Application US/08440549
; Patent No. 6312889
; GENERAL INFORMATION:
; APPLICANT: Houghton, Michael
; APPLICANT: Choo, Qui-Lim
; APPLICANT: Kuo, George
; TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV)
; TITLE OF INVENTION: Antigens for Use in Immunoassays for Anti-HCV Antibodies
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: P.O. Box 8097 (Int. Prop. R-440)
; CITY: Emeryville
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/440,549
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/910,760
; FILING DATE: 07-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Blackburn Esq., Robert P.
; REGISTRATION NUMBER: 30,447
; REFERENCE/DOCKET NUMBER: 0101.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2702
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3011 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-440-549-10

Query Match 99.5%; Score 1035; DB 3; Length 3011;
Best Local Similarity 99.5%; Pred. No. 1.1e-90;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKPKKKNTNRRPDVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
DB 1 MSTNPKPKKKNTNRRPDVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
QY 61 RRQIPKARRPEGRGRTWAQGYWPPLYGNECGWAGWLLSPRGSRPSWGPTDPRRRRNLG 120
DB 61 RRQIPKARRPEGRGRTWAQGYWPPLYGNECGWAGWLLSPRGSRPSWGPTDPRRRRNLG 120
QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPVAGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191

RESULT 12
US-08-850-328-1
; Sequence 1, Application US/08850328
; Patent No. 6379886
; GENERAL INFORMATION:
; APPLICANT: TAKAHAMA, Y.
; APPLICANT: SHIRAIISHI, J.
; TITLE OF INVENTION: DIAGNOSTIC REAGENT FOR HEPATITIS
; TITLE OF INVENTION: C VIRUS INFECTION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,328
; FILING DATE: 02-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mays, Thomas D

; APPLICATION NUMBER: 34,524
; REFERENCE/DOCKET NUMBER: 32273-20004.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3011 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-850-328-1

Query Match 99.5%; Score 1035; DB 3; Length 3011;
Best Local Similarity 99.5%; Pred. No. 1.1e-90;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKPKKKNTNRRPDVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
DB 1 MSTNPKPKKKNTNRRPDVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
QY 61 RRQIPKARRPEGRGRTWAQGYWPPLYGNECGWAGWLLSPRGSRPSWGPTDPRRRRNLG 120
DB 61 RRQIPKARRPEGRGRTWAQGYWPPLYGNECGWAGWLLSPRGSRPSWGPTDPRRRRNLG 120
QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPVAGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191

RESULT 13
US-09-916-359-2
; Sequence 2, Application US/09916359
; Patent No. 6538123
; GENERAL INFORMATION:
; APPLICANT: Veronique Barban
; TITLE OF INVENTION: VACCINE COMPOSITION FOR PREVENTING OR
; TITLE OF INVENTION: TREATING C HEPATITIS
; FILE REFERENCE: PMCF97-03A
; CURRENT APPLICATION NUMBER: US/09/916,359
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 09/388,874
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 97/02,887
; PRIOR FILING DATE: 1997-03-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3011
; TYPE: PRT
; ORGANISM: Virus
; US-09-916-359-2

Query Match 99.5%; Score 1035; DB 4; Length 3011;
Best Local Similarity 99.5%; Pred. No. 1.1e-90;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKPKKKNTNRRPDVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
DB 1 MSTNPKPKKKNTNRRPDVKFPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
QY 61 RRQIPKARRPEGRGRTWAQGYWPPLYGNECGWAGWLLSPRGSRPSWGPTDPRRRRNLG 120
DB 61 RRQIPKARRPEGRGRTWAQGYWPPLYGNECGWAGWLLSPRGSRPSWGPTDPRRRRNLG 120
QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLA 180
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Db 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191

Db 181 LLSCLTVPASA 191

RESULT 14

US-07-681-703B-12

; Sequence 12, Application US/07681703B

; Patent No. 5443965

; GENERAL INFORMATION:

; APPLICANT: Reyes, Gregory

; APPLICANT: Kim, Jungshuh P.

; APPLICANT: Moeckli, Randolph

; TITLE OF INVENTION: Hepatitis C Virus Epitopes

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: 350 Cambridge Ave., Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/681,703B

; FILING DATE: 05-APR-1991

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 505,611

; FILING DATE: 06-APR-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 594,854

; FILING DATE: 09-OCT-1990

; NAME: Fabian, Gary R.

; REGISTRATION NUMBER: 33,875

; REFERENCE/DOCKET NUMBER: 4600-076.21

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0880

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 215 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-07-681-703B-12

Query Match 99.1%; Score 1031; DB 1; Length 215;

Best Local Similarity 99.0%; Pred. No. 1.1e-91;

Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNTNRRPQDVKPGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60

Db 1 MGTNPKQKKNTNRRPQDVKPGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60

Qy 61 RRQPIPKARREGETWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRSRLG 120

Db 61 RRQPIPKARREGETWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRSRLG 120

Qy 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180

Db 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180

Qy 181 LLSCLTVPASA 191

Db 181 LLSCLTVPASA 191

Search completed: August 19, 2005, 12:44:52

Job time : 21 secs

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OM protein - protein search, using sw model

Run on: August 19, 2005, 12:28:45 ; Search time 117.5 Seconds
(without alignments)
628.691 Million cell updates/sec

Title: US-10-770-117-2

Perfect score: 1040

Sequence: 1 MSTNPKQKGNKNTNRPO.....CSPSIFLLALLSCLTVPASA 191

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1040	100.0	191	3	AAY82997 Hepatitis
2	1035	99.5	191	3	AAY82999 Hepatitis
3	1035	99.5	2816	2	AAR34009 HCV-1 pol
4	1035	99.5	2955	2	AAY14975 Amino aci
5	1035	99.5	2955	3	AAB18541 Polypeptide
6	1035	99.5	3011	2	AAR21519 Compiled
7	1035	99.5	3011	2	AAR90931 Hepatitis
8	1035	99.5	3011	2	AAR34480 HCV polyp
9	1035	99.5	3011	2	AAR40038 HCV polyp
10	1035	99.5	3011	5	AAR22049 Hepatitis
11	1035	99.5	3011	8	ADL23107 Hepatitis
12	1035	99.5	3011	8	ADR29357 Hepatitis
13	1031	99.1	190	7	ADE39661 Hepatitis
14	1031	99.1	215	2	AAR14557 HCV Capsi
15	1031	99.1	215	2	AAR14558 Polypepti
16	1031	99.1	215	2	AAR81945 Hepatitis
17	1031	99.1	215	2	AAR81944 Hepatitis
18	1031	99.1	217	2	AAR70828 Hepatitis
19	1031	99.1	217	2	AAR70829 Insert of
20	1031	99.1	217	2	AAR80517 HCV type
21	1031	99.1	217	2	AAR80516 Hepatitis
22	1030	99.0	190	5	AAB71256 HCV cDNA
23	1030	99.0	2955	8	ADN35978 HCV cDNA
24	1026	98.7	191	2	AAR44010 Hepatitis
25	1026	98.7	191	2	AAR92938 Hepatitis

ALIGNMENTS

RESULT 1

AAY82997

ID AAY82997 standard; peptide; 191 AA.

XX AAY82997;

AC AAY82997;

XX AAY82997;

DT 04-JUL-2000 (first entry)

XX AAY82997;

DE Hepatitis C virus core polypeptide having Leu to Ala substitution.

XX Hepatitis C virus; HCV; core polypeptide; antigen; epitope; agraetope;

KW anchor residue; cytotoxic T lymphocyte; CTL; immune response; MHC;

KW Major histocompatibility complex; vaccine; treatment.

XX Synthetic.

OS Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

XX Hepatitis C virus; (HCV).

CC they are bound and presented by. The motifs are based on the presence in
 CC precise positions in the peptide sequence of several amino acids
 CC (agretropic residues) called anchor residues, responsible for interactions
 CC between peptide and MHC molecule, as well as other secondary position
 CC that may help to stabilise the interaction. Thus, single amino acid
 CC changes within the peptide sequence can enhance the immune response.
 CC Peptides derived from the HCV core polypeptide having substituted amino
 CC acids within their sequence, specifically a hepatitis C virus core
 CC polypeptide comprising an L to an A substitution at amino acid position
 CC 139 enhance the immune response against HCV. They can therefore be used
 CC as a vaccine or for treating HCV infection

XX Sequence 191 AA;

Query Match 100.0%; Score 1040; DB 3; Length 191;
 Best Local Similarity 100.0%; Pred. No. 2.7e-91;
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTNPKPKKNTNRRPQDVKFGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
 DB 1 MSTNPKPKKNTNRRPQDVKFGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
 QY 61 RRQPIPKARPEGRGRTWAQPGYWPPLYGNECGWAGWLLSPRGSRPWSGPTDPRRSRNLG 120
 DB 61 RRQPIPKARPEGRGRTWAQPGYWPPLYGNECGWAGWLLSPRGSRPWSGPTDPRRSRNLG 120
 QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEGDVNYATGNLPGCSFSIFLLA 180
 DB 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEGDVNYATGNLPGCSFSIFLLA 180
 QY 181 LLSCLTVPASA 191
 DB 181 LLSCLTVPASA 191

RESULT 2

AA82999 standard; peptide; 191 AA.

XX AC

XX AC

DT 12-SEP-2003 (revised)

DT 04-JUL-2000 (first entry)

XX Hepatitis C virus core polypeptide.

XX Hepatitis C virus; HCV; core polypeptide; antigen; epitope; agretope;

XX anchor residue; cytotoxic T lymphocyte; CTL; immune response; MHC;

XX Major histocompatibility complex; vaccine; treatment.

XX Hepatitis C virus; (HCV).

XX WO200011186-A1.

XX 02-MAR-2000.

XX 17-AUG-1999; 99WO-US018674.

XX 21-AUG-1998; 98US-0097446P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Berzofsky JA, Sarobe P, Pendleton CD, Feinstein SM, Arichi T;

XX Major ME;

XX WPI; 2000-246569/21.

XX Hepatitis C virus polypeptides is useful as a vaccine for treating

PT Hepatitis C virus infection and for activating cytotoxic T lymphocytes.

XX Disclosure; Page 72-73; 78pp; English.

XX Peptide fragments of the Hepatitis C virus (HCV) core polypeptide can be

CC used to elicit an immune response. A cytotoxic T-lymphocyte (CTL)
 CC response is present in patients acutely and chronically infected by HCV.
 CC CTL's recognise viral antigens as peptides presented by Class I molecules
 CC of the major histocompatibility complex (MHC). These peptide antigens are
 CC typically 8-10 amino acids long. These peptide antigens typically have a
 CC sequence pattern or motif depending upon which particular MHC antigen
 CC they are bound and presented by. The motifs are based on the presence in
 CC precise positions in the peptide sequence of several amino acids
 CC (agretropic residues) called anchor residues, responsible for interactions
 CC between peptide and MHC molecule, as well as other secondary position
 CC that may help to stabilise the interaction. Thus, single amino acid
 CC changes within the peptide sequence can enhance the immune response.
 CC Peptides derived from the HCV core polypeptide having substituted amino
 CC acids within their sequence, specifically a hepatitis C virus core
 CC polypeptide comprising an L to an A substitution at amino acid position
 CC 139 enhance the immune response against HCV. They can therefore be used
 CC as a vaccine or for treating HCV infection. (Updated on 12-SEP-2003 to
 CC standardise OS field)

XX Sequence 191 AA;

Query Match 99.5%; Score 1035; DB 3; Length 191;
 Best Local Similarity 99.5%; Pred. No. 8.1e-91;
 Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKPKKNTNRRPQDVKFGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
 DB 1 MSTNPKPKKNTNRRPQDVKFGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
 QY 61 RRQPIPKARPEGRGRTWAQPGYWPPLYGNECGWAGWLLSPRGSRPWSGPTDPRRSRNLG 120
 DB 61 RRQPIPKARPEGRGRTWAQPGYWPPLYGNECGWAGWLLSPRGSRPWSGPTDPRRSRNLG 120
 QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEGDVNYATGNLPGCSFSIFLLA 180
 DB 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRVLEGDVNYATGNLPGCSFSIFLLA 180
 QY 181 LLSCLTVPASA 191
 DB 181 LLSCLTVPASA 191

RESULT 3

AA834009 standard; protein; 2816 AA.

XX AC

XX AC

DT 25-MAR-2003 (revised)

DT 26-JUL-1993 (first entry)

XX HCV-1 polypeptide.

XX XX

XX Polymerase chain reaction; PCR; amplify; primer; hepatitis C virus; HCV;

XX asymptomatic; chronically infected; epitope; viral isolate; domain;

XX immunological; cross-reactive; envelope protein; vaccine;

XX gp53 (BVDV)/gp55; hog cholera virus; pestivirus; NS1; flavivirus.

XX Hepatitis C virus.

XX WO9306126-A1.

XX 01-APR-1993.

XX 11-SEP-1992; 92WO-US007683.

XX 13-SEP-1991; 91US-00759575.

XX (CHIR) CHIRON CORP.

XX Weiner AJ, Houghton M;

XX WPI; 1993-117468/14.

XX Immuno-reactive hepatitis C virus polypeptide compsns. - contg. at least
PT 2 sequences from the first variable domain of distinct HCV isolates.
XX
XX Disclosure; Fig 9; 106pp; English.
XX
XX This sequence represents the entire hepatitis C virus polypeptide. HCV is
CC a member of the flavivirus family and appears to encode a basic
CC polypeptide domain ("C") at the N-terminal of the viral polypeptide,
CC followed by two glycoprotein domains ("E1", "E2/NS1"), upstream of the
CC nonstructural genes NS2 through NS5. See also AAQ39134-48, AAQ33982- 4008
CC and AAQ38088-89. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 2816 AA;

Query Match 99.5%; Score 1035; DB 2; Length 2816;
Best Local Similarity 99.5%; Pred. No. 1.8e-89;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNKNTNRRPQDVKPGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60
DB 1 MSTNPKQKKNKNTNRRPQDVKPGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60
|||||
QY 61 RRQPIPKARPEGRTPAQPGYPWPPLYGNEGCGWAGLLSPRGSRPSPGPTDPRRRSRNLG 120
DB 61 RRQPIPKARPEGRTPAQPGYPWPPLYGNEGCGWAGLLSPRGSRPSPGPTDPRRRSRNLG 120
|||||
QY 121 KVIDTLTCGFADLMGYIPAVCAPLGGAAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPAVCAPLGGAAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
|||||
QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191
|||||

RESULT 4
AA14975
ID AA14975 standard; protein; 2955 AA.
XX
XX AA14975;
XX
XX 20-MAR-2003 (revised)
DT 08-NOV-1999 (first entry)
XX
XX Amino acid sequence of HCV-1 ORF.
XX
XX Hepatitis C virus; HCV; J1; J7; HCV-1; non-A, non-B HCV; NANBH;
KW HCV infection; vaccine.
XX
XX Hepatitis C virus.
XX
XX Key Location/Qualifiers
FH Misc-difference 441
FT /note= "encoded by TT"
FT Misc-difference 461
FT /note= "encoded by CCCC"
XX
XX EP39128-A2.
XX
XX 01-SEP-1999.
XX
XX 17-SEP-1990; 99EP-00101746.
XX
XX 15-SEP-1989; 89US-00408045.
PR 21-DEC-1989; 89US-00456142.
PR 17-SEP-1990; 90EP-00310149.
XX
XX (OYAA/) OYA A.
PA (CHIR) CHIRON CORP.
XX
XX Miyamura T, Saito I, Houghton M, Weiner AJ, Han J, Kolberg JA;
PI Cha T, Irvine BD;

XX WPI; 1999-480843/41.
DR N-PSDB; AAQ07656.
XX
XX New Hepatitis C Virus isolates, useful for diagnosis of hepatitis
PT infections and development of vaccines.
XX
XX Disclosure; Fig 12; 132pp; English.
XX
XX The invention provides two new isolates of hepatitis C virus (HCV), J1
CC and J7. These two isolates comprise nucleotide and amino acid sequences
CC that are distinct from the HCV isolate HCV-1. The nucleotide sequences
CC may be used to detect non-A, non-B HCV (NANBH) polynucleotides by
CC hybridization for diagnosis of NANBH infections. They may also be used to
CC screen blood donors, donated blood and blood products for this infection.
CC The isolates may also be used to isolate other naturally occurring
CC variants of the virus. The polypeptides may be used as a vaccine for
CC administration to patients to protect against infection with NANBH. The
CC present sequence represents the amino acid sequence of HCV-1 ORF.
CC (Updated on 20-MAR-2003 to correct PF field.) (Updated on 20-MAR-2003 to
CC correct PR field.)
XX
SQ Sequence 2955 AA;

Query Match 99.5%; Score 1035; DB 2; Length 2955;
Best Local Similarity 99.5%; Pred. No. 1.9e-89;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNKNTNRRPQDVKPGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60
DB 1 MSTNPKQKKNKNTNRRPQDVKPGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60
|||||
QY 61 RRQPIPKARPEGRTPAQPGYPWPPLYGNEGCGWAGLLSPRGSRPSPGPTDPRRRSRNLG 120
DB 61 RRQPIPKARPEGRTPAQPGYPWPPLYGNEGCGWAGLLSPRGSRPSPGPTDPRRRSRNLG 120
|||||
QY 121 KVIDTLTCGFADLMGYIPAVCAPLGGAAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
DB 121 KVIDTLTCGFADLMGYIPAVCAPLGGAAARALAHGVRVLEGGVNYATGNLPGCSFSIFLLA 180
|||||
QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191
|||||

RESULT 5
AA18541
ID AA18541 standard; protein; 2955 AA.
XX
XX AA18541;
XX
XX 15-JAN-2001 (first entry)
XX
XX Polypeptide encoded by sense strand of HCV.
XX
XX Hepatitis C virus; HCV; antisense polynucleotide; polypeptide;
KW viral infectivity; viral replication.
XX
XX Hepatitis C virus.
XX
XX EP1034785-A2.
XX
XX 13-SEP-2000.
XX
XX 16-MAR-1990; 2000EP-00109602.
XX
XX 17-MAR-1989; 89US-00325338.
PR 20-APR-1989; 89US-00341334.
PR 18-MAY-1989; 89US-00355002.
PR 16-MAR-1990; 90EP-00302866.
XX
XX (CHIR) CHIRON CORP.
PA
XX

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PI Houghton M, Choo Q, Kuo G;
XX WPI; 2000-566891/53.
DR N-PSDB; AAA75297.
XX
XX Novel composition comprising a hepatitis C virus antisense polynucleotide
XX which is complementary to or corresponds to a sense strand of the virus
XX genome, and selectively hybridizes to it.
XX
XX Example; Fig 17; 75pp; English.
XX
XX The specification describes a pharmaceutical composition which comprises
XX a hepatitis C virus (HCV) antisense polynucleotide. The HCV is
XX characterized by a positive stranded RNA genome which has 40% homology at
XX the polypeptide level to a HCV polyprotein. The antisense polynucleotide
XX binds to cellular polynucleotides which enhance and/or are required for
XX viral infectivity, replicative ability or chronicity. The antisense
XX polynucleotides may also be designed to bind with high specificity, to be
XX of increased stability, to be stable and to have low toxicity. The
XX composition also comprises an agent which causes viral RNA to be
XX inactive. The composition is used for preventing HCV replication in a
XX system. The present sequence is encoded by a novel HCV CDNA sequence,
XX which is used in the course of the invention
XX
XX Sequence 2955 AA;
SQ
Query Match 99.5%; Score 1035; DB 3; Length 2955;
Best Local Similarity 99.5%; Pred. No. 1.9e-89;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSTNPKPKKKNTNRNRRPQDVKPGGGQIVGGVYLLPRGGPRLGVRATKTSERSQPRG 60
DB 1 MSTNPKPKKKNTNRNRRPQDVKPGGGQIVGGVYLLPRGGPRLGVRATKTSERSQPRG 60
QY 61 RRQIPKARPEGTWAPQGYPMPLYNCGCGWAGMLLSPRSGRPSWGPTDPRRSRNLG 120
DB 61 RRQIPKARPEGTWAPQGYPMPLYNCGCGWAGMLLSPRSGRPSWGPTDPRRSRNLG 120
QY 121 KVDTLTGCGFADLMGYITPAGVAPLGGAAALAHGVRVLEDGVNATGNLPGCSFSIFLLA 180
DB 121 KVDTLTGCGFADLMGYITPAGVAPLGGAAALAHGVRVLEDGVNATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
DB 181 LLSCLTVPASA 191
RESULT 6
AAR21519
ID AAR21519 standard; protein; 3011 AA.
XX
XX AAR21519;
AC
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 22-JUN-1992 (first entry)
XX
XX Compiled HCV sequence.
DE
XX HCV1; serum; gt11.
KW
XX Hepatitis C virus type 1.
OS
XX Key Location/Qualifiers
FH Misc-difference 9 /label= ARG
FT Misc-difference 11 /label= THR
FT Misc-difference 176 /label= THR
FT Misc-difference 334 /label= VAL
FT Misc-difference 603

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FT Misc-difference 848 /label= ILE
FT Misc-difference 1114 /label= (ASN)
FT Misc-difference 1117 /label= SER
FT Misc-difference 1276 /label= THR
FT Misc-difference 1328 /label= LEU
FT Misc-difference 1454 /label= (VAL)
FT Misc-difference 1471 /label= TYR
FT Misc-difference 1877 /label= (SER)
FT Misc-difference 1948 /label= (GLY)
FT Misc-difference 1949 /label= (HIS)
FT Misc-difference 2021 /label= (CYS)
FT Misc-difference 2349 /label= (VAL)
FT Misc-difference 2385 /label= (SER)
FT Misc-difference 2386 /label= (PHE)
FT Misc-difference 2502 /label= (ALA)
FT Misc-difference 2690 /label= (PHE)
FT Misc-difference 2996 /label= (GLY)
FT Misc-difference 2996 /label= (PRO)
XX
XX WO9202642-A.
XX
XX 20-FEB-1992.
XX
XX 10-AUG-1990; 90US-00566209.
XX
XX 10-AUG-1990; 90US-00566209.
XX (CHIR ) CHIRON CORP.
XX
XX Houghton M, Choo QL, Kuo G, Weiner AJ, Uredea MS, Irvine BD;
XX Kolberg JA;
XX WPI; 1992-080094/10.
XX N-PSDB; AAQ21744.
XX
XX Reagents for isolating, amplifying and detecting HCV polynucleotide(s) -
XX used to monitor spread of blood-borne non-a, non-b hepatitis virus
XX infection and screen blood samples for virus.
XX
XX Disclosure; Fig 1; 67pp; English.
XX
XX Heterogeneities in cloned DNAs of HCV1 are indicated by the amino acid
XX indicated in the features, the parentheses indicated that the
XX heterogeneity was detected at or near to the 5'- or 3'-end of the HCV in
XX the clone. The sequence is derived from a composite HCV cDNA from HCV1, a
XX prototypic HCV. The DNA sequence is based upon sequence information
XX derived from a no. of HCV cDNA clones, which were isolated from a no. of
XX HCV cDNA libraries, including the "c" library present in lambda gt11
XX (ATCC No.40394), and from human serum. The HCV cDNA clones were isolated
XX by methods described in WO9014436. The clones from which the sequence was
XX derived are 5'clone32, b114a, 18g, ag30a, CA205a, CA290a, CA216a, p114a,
XX CA167b, CA156e, CA84a, CA59a, K9-1 (also called k9-1), 26j, 13i, 12f, 8f,
XX 14i, 11b, 7f, 7e, 8h, 33c, 40b, 37b, 35, 36, 8i, 32, 33b, 25c, 14c, 8f,
XX 33f, 33g, 33c, 35f, 19g, 26g, 15e, b5a, 16jh, 6k and p131jh. (Updated on
XX 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
XX field.) (Updated on 24-OCT-2003 to standardise OS field)

```

```
XX SQ Sequence 3011 AA;
Query Match 99.5%; Score 1035; DB 2; Length 3011;
Best Local Similarity 99.5%; Pred. No. 1.9e-89;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNKNTNRRPQDVKPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKQKKNKNTNRRPQDVKPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Qy 61 RRQPIPKARRPEGRTPWQPGYPWPLYGNEGCGWAGWLLSPRSGRPSWGPTDPRRRSRNLG 120
Db 61 RRQPIPKARRPEGRTPWQPGYPWPLYGNEGCGWAGWLLSPRSGRPSWGPTDPRRRSRNLG 120
Qy 121 KVDTLTTCGADLMGYIPAVGAPLGGAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180
Db 121 KVDTLTTCGADLMGYIPAVGAPLGGAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180
Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 7
ID AAR90931 standard; protein; 3011 AA.
XX
AC AAR90931;
XX
DT 25-MAR-2003 (revised)
DT 15-MAY-1996 (first entry)
XX
DE Hepatitis C virus polyprotein.
XX
KW Non-A non-B hepatitis virus; NANBHV; HCV; antigen; detection; diagnosis;
KW antibodies.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..122
FT /label= antigen
FT /note= "C22; AAR90936"
FT Misc-difference 199..328
FT /label= antigen
FT /note= "S2; AAR90935"
FT Misc-difference 1192..1457
FT /label= antigen
FT /note= "C33C; AAR90932"
FT Misc-difference 1569..1931
FT /label= antigen
FT /note= "C100; AAR90933"
FT Misc-difference 2054..2464
FT /label= antigen
FT /note= "NS5; AAR90934"
XX
FN EP693687-A1.
XX
XX 24-JAN-1996.
XX
XX 03-APR-1991; 95EP-00114016.
XX
XX 04-APR-1990; 90US-00504352.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Houghton M, Choo Q, Kuo G;
XX
XX WPI; 1996-117956/13.
XX
XX N-PSDB; AAT12710.
XX
XX Combinations of synthetic Hepatitis C Virus antigens - provide more
```

```
PT effective diagnosis of Non-A, Non-B Hepatitis.
XX Disclosure; Fig 1(A-Y); 53pp; English.
XX
CC The combination comprises an HCV antigen from the C domain (pref. C22 -
CC AAR90936) and at least one HCV antigen from the NS3 (pref. C33c -
CC AAR90932), NS4 (pref. C100 - AAR90933), S (pref. S2 - AAR90933) or NS5
CC (AAR90934) domain. The antigens may in the form of a fusion protein, a
CC simple physical mixture, or the individual antigens commonly bound to a
CC solid matrix. They are pref. prepd. by recombinant DNA techniques
CC (primers are given in AAT12711-T12716), but can be synthesised or
CC isolated from HCV using affinity chromatography. (Updated on 25-MAR-2003
CC to correct PF field.)
XX
SQ Sequence 3011 AA;
Query Match 99.5%; Score 1035; DB 2; Length 3011;
Best Local Similarity 99.5%; Pred. No. 1.9e-89;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSTNPKQKKNKNTNRRPQDVKPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPKQKKNKNTNRRPQDVKPGGGQIVGGVYLLPRGPRLGVRATKTSERSQPRG 60
Qy 61 RRQPIPKARRPEGRTPWQPGYPWPLYGNEGCGWAGWLLSPRSGRPSWGPTDPRRRSRNLG 120
Db 61 RRQPIPKARRPEGRTPWQPGYPWPLYGNEGCGWAGWLLSPRSGRPSWGPTDPRRRSRNLG 120
Qy 121 KVDTLTTCGADLMGYIPAVGAPLGGAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180
Db 121 KVDTLTTCGADLMGYIPAVGAPLGGAARALAHGVRVLEGVNATGNLPGCSFSIFLLA 180
Qy 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

RESULT 8
AAW34480
ID AAW34480 standard; protein; 3011 AA.
XX
AC AAW34480;
XX
DT 25-MAR-2003 (revised)
DT 16-MAR-1998 (first entry)
XX
DE HCV polyprotein.
XX
KW PCR primer; amplif; HCV; hepatitis c virus; antigen combination; NS3;
KW C domain; S domain; NS5; HCV polyprotein; anti-HCV antibody; detection;
KW NS4.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 366
FT /note= "can optionally be Arg"
FT Misc-difference 372
FT /note= "can optionally be Thr"
FT Misc-difference 867
FT /note= "can optionally be Thr"
FT Misc-difference 1341
FT /note= "can optionally be Val"
FT Misc-difference 2148
FT /note= "can optionally be Ile"
FT Misc-difference 2883
FT /note= "can optionally be Asn"
FT Misc-difference 3691
FT /note= "can optionally be Ser"
FT Misc-difference 3690
FT /note= "can optionally be Thr"
FT Misc-difference 4167
FT /note= "can optionally be Leu"
```

[illegible]

FT also be Leu"
FT 1328 Modified-site /note= "As given in the specification this amino acid can
FT also be Val"
FT 1452 Modified-site /note= "As given in the specification this amino acid can
FT also be Tyr"
FT 1472 Modified-site /note= "As given in the specification this amino acid can
FT also be Ser"
FT 1640 Domain /label= NS4_domain
FT 1877 Modified-site /note= "As given in the specification this amino acid can
FT also be Gly"
FT 1948 Modified-site /note= "As given in the specification this amino acid can
FT also be His"
FT 1949 Modified-site /note= "As given in the specification this amino acid can
FT also be Cys"
FT 2000 Domain /label= NS5_domain
FT 2021 Modified-site /note= "As given in the specification this amino acid can
FT also be Val"
FT 2348 Modified-site /note= "As given in the specification this amino acid can
FT also be Ser"
FT 2385 Modified-site /note= "As given in the specification this amino acid can
FT also be Phe"
FT 2386 Modified-site /note= "As given in the specification this amino acid can
FT also be Ala"
FT 2502 Modified-site /note= "As given in the specification this amino acid can
FT also be Phe"
FT 2690 Modified-site /note= "As given in the specification this amino acid can
FT also be Gly"
FT 2921 Modified-site /note= "As given in the specification this amino acid can
FT also be Gly"
FT 2996 Modified-site /note= "As given in the specification this amino acid can
FT also be Pro"
XX US5712087-A.
PN
XX
XX
PD 27-JAN-1998.
XX
XX 12-MAY-1995; 95US-00440519.
XX
XX 04-APR-1990; 90US-00504352.
PR 07-JUL-1992; 92US-00910760.
XX
XX (CHIR) CHIRON CORP.
XX
XX Kuo G, Houghton M, Choo Q;
XX WPI, 1998-119973/11.
DR N-PSDB; AAV09989.
XX
XX Immunassays for hepatitis C virus antibodies - using combinations of
FT antigenic fragments of HCV polyprotein.
XX
XX Disclosure; Fig 1; 59pp; English.
XX
XX This sequence represents the hepatitis C virus (HCV) polyprotein which is
CC used in the construction of novel combinations of HCV antigens that have
CC a broader range of immunological activity than any single HCV antigen. An
CC example of such an antigen given in this specification comprises a first

CC antigen containing at least 8 amino acids of the C domain of the HCV
CC polyprotein and a second antigen comprising at least 8 amino acids of the
CC NS3 domain, the NS4 domain, the S domain or the NS5 domain of the HCV
CC polyprotein in the form of a fusion protein, a physical mixture or bound
CC to a solid matrix. Note: The features given in the specification as
CC represented in the feature table of AAW40038 differ from the positions
CC indicated in Figure 1
XX
SQ Sequence 3011 AA;
Query Match 99.5%; Score 1035; DB 2; Length 3011;
Best Local Similarity 99.5%; Pred. No. 1.9e-89;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MSTNPQPKKNKNTNRRPDQVKFGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60
Db 1 MSTNPQPKKNKNTNRRPDQVKFGGQIVGGVYLLPRRGPRLGVRATKTSERSQPRG 60
Qy 61 RRQPIPKARRPEGRWQAQPGYPWPLYGNEGCGWAGLLSPRGSRPSWGPTDPRRRRNLG 120
Db 61 RRQPIPKARRPEGRWQAQPGYPWPLYGNEGCGWAGLLSPRGSRPSWGPTDPRRRRNLG 120
Qy 121 KVDTTTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVDTTTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
Qy 181 LLSCLTVPSA 191
Db 181 LLSCLTVPSA 191
RESULT 10
AAE22049
ID AAE22049 standard; protein; 3011 AA.
XX
AC AAE22049;
XX
XX 16-JUL-2002 (first entry)
DT
XX
XX Hepatitis C virus (HCV) polyprotein.
DE
XX
XX Hepatitis C virus; HCV; antigen; C domain; polyprotein; NS3 domain;
KW NS4 domain; S domain; NS5 domain.
XX
XX Hepatitis C virus.
OS
XX
XX Key Location/Qualifiers
FH Domain 1. .122
FT /label= C domain
FT Domain 199. .328
FT /label= S domain
FT Region 1192. .1931
FT /note= "c200 polypeptide"
FT Region 1192. .1457
FT /note= "NS3 domain antigen"
FT Region 1569. .1931
FT /note= "NS4 antigen"
FT Region 2054. .2464
FT /note= "NS5 antigen"
XX
XX US6312889-B1.
XX
XX
XX 06-NOV-2001.
PD
XX
XX 12-MAY-1995; 95US-00440549.
XX
XX 04-APR-1990; 90US-00504352.
PR 07-JUL-1992; 92US-00910760.
XX
XX (CHIR) CHIRON CORP.
XX
XX Houghton M, Choo Q, Kuo G;
XX
XX

DR WPI; 2002-040268/05.
XX N-PSDB; AAD35043.
PT Combination of hepatitis C viral (HCV) antigens, useful in improved
XX immunoassay for detecting HCV antibodies.
PS Example 1; Col 45-60; 58pp; English.
XX
CC The invention relates to combination of hepatitis C viral (HCV) antigens
CC that have a broader range of immunological reactivity than any single HCV
CC antigen. The combinations consist of an antigen from the C domain of the
CC HCV polyprotein, and at least one additional HCV antigen from either the
CC NS3 domain, the NS4 domain, the S domain, or the NS5 domain and are in
CC the form of fusion protein, a simple physical mixture, or the individual
CC antigens commonly bound to a solid matrix. The combinations of antigens
CC provides broad range immunoassays for anti-HCV antibodies. The invention
CC therefore provides a method for detecting antibodies to HCV in a mammal
CC suspected of containing such antibodies. The present sequence is HCV
CC polyprotein. Note: This sequence SEQ.ID.NO:10 is stated to be similar to
CC the sequence shown in Fig 1 (AAB22052) of the specification. However
CC these sequences differ
XX
SQ Sequence 3011 AA;
Query Match 99.5%; Score 1035; DB 5; Length 3011;
Best Local Similarity 99.5%; Pred. No. 1.9e-89;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSTNPKQKKNKNTNRRPQDVKFGGGQIVGGVYLLPRRGLGVRATKTSERSQPRG 60
Db 1 MSTNPKQKKNKNTNRRPQDVKFGGGQIVGGVYLLPRRGLGVRATKTSERSQPRG 60
QY 61 RRQPIKARPEGRGRTWAQPGYWPPLYGNECGWAGWLLSPRGSRPSWGPTDPRRRNLG 120
Db 61 RRQPIKARPEGRGRTWAQPGYWPPLYGNECGWAGWLLSPRGSRPSWGPTDPRRRNLG 120
QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPVPLVGAAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191
RESULT 11
ADL23107
ID ADL23107 standard; protein; 3011 AA.
XX
XX ADL23107;
AC
XX 20-MAY-2004 (first entry)
DT
XX
XX Hepatitis C virus protein sequence Seqid 2.
DE
XX hepatitis C virus; HCV; viral envelope; E2 glycoprotein;
KW low density lipoprotein; LDL; HCV infection; hypercholesterolaemia;
KW hyperlipidaemia; coronary heart disease; hepatotropic; virucidal;
KW plasma lipoprotein.
XX
XX Hepatitis C virus.
OS
XX
XX WO2004003141-A2.
PN
XX
XX 08-JAN-2004.
PD
XX
XX 24-JUN-2003; 2003WO-US019834.
PP
XX
XX 28-JUN-2002; 2002US-0392158P.
PR
XX
XX 27-MAY-2003; 2003US-00445724.
XX
XX (IOWA) UNIV IOWA RES FOUND.
PA
XX

PI Stapleton JT, Wuenschmann S;
XX
DR WPI; 2004-083029/08.
DR N-PSDB; ADL23106.
XX
XX Use of Hepatitis C Virus E2 glycoprotein in reducing low density
PT lipoprotein levels in a subject or in treating or preventing hepatitis C
PT virus infection.
PT
XX
XX Disclosure; SEQ ID NO 2; 135pp; English.
PS
XX This invention relates to a novel method for identifying inhibitors of
XX the hepatitis C virus (HCV), and also the use of an HCV viral envelope
CC protein identified as E2 glycoprotein in reducing low density lipoprotein
CC (LDL) levels. Specifically, it refers to the knowledge that HCV E2
CC glycoprotein binds to the lipid moiety of human lipoproteins and uses the
CC natural LDL receptor to bind to cells, thus identifies a novel route by
CC which HCV gains entry to the cell providing a novel therapeutic target.
CC The present invention describes screening methods to identify inhibitors
CC of HCV infection that comprises admixing a candidate substance with the
CC E2 glycoprotein and a plasma lipoprotein in order to determine a
CC reduction in binding in the presence of an appropriate inhibitor. As
CC such, these compositions can be used to reduce hypercholesterolaemia and
CC in turn treat hyperlipidaemia and associated conditions including
CC coronary heart disease. Accordingly, they exhibit hepatotropic and
CC virucidal activities. This polypeptide sequence is the HCV protein
CC sequence of the invention.
XX
SQ Sequence 3011 AA;
Query Match 99.5%; Score 1035; DB 8; Length 3011;
Best Local Similarity 99.5%; Pred. No. 1.9e-89;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSTNPKQKKNKNTNRRPQDVKFGGGQIVGGVYLLPRRGLGVRATKTSERSQPRG 60
Db 1 MSTNPKQKKNKNTNRRPQDVKFGGGQIVGGVYLLPRRGLGVRATKTSERSQPRG 60
QY 61 RRQPIKARPEGRGRTWAQPGYWPPLYGNECGWAGWLLSPRGSRPSWGPTDPRRRNLG 120
Db 61 RRQPIKARPEGRGRTWAQPGYWPPLYGNECGWAGWLLSPRGSRPSWGPTDPRRRNLG 120
QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPVPLVGAAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191
RESULT 12
ADR29357
ID ADR29357 standard; protein; 3011 AA.
XX
XX ADR29357;
AC
XX
XX 18-NOV-2004 (first entry)
DT
XX
XX Hepatitis C virus polyprotein precursor protein SEQ ID NO:1.
DE
XX anti-hepatitis C virus; anti-HCV; immune response; anti-HIV; virucide;
KW antinflammatory; hepatotropic; immunostimulant; vaccine; immunotherapy;
KW anti-HCV vaccine; AIDS; hepatitis C virus; HCV; polyprotein precursor.
XX
XX Hepatitis C virus.
OS
XX
XX Key Location/Qualifiers
FH Key 2594..2602
FT Peptide /note= "specifically claimed peptide in claims 4 and 5"
XX
XX WO2004071414-A2.
PN
XX

PD 26-AUG-2004.
 XX 03-FEB-2004; 2004WO-US003044.
 PF 05-FEB-2003; 2003US-0445438P.
 PR 25-MAR-2003; 2003US-0457870P.
 XX (GENZ) GENZYME CORP.
 PA (GENO) GEN HOSPITAL CORP DBA MASSACHUSETTS GEN.
 XX Nicolette CA, Walker BD;
 PI WPI; 2004-625761/60.
 XX N-PSDB; ADR29358.
 DR GENBANK; M62321.
 XX New anti- hepatitis C virus (HCV) (AL9) compound, useful as component of
 PT anti-HCV vaccines and to expand immune effector cell specific for cells
 PT expressing HCV epitope.
 XX Claim 4; SEQ ID NO 1; 69pp; English.
 PS
 XX The present invention describes anti-hepatitis C virus (HCV) (AL9)
 CC compounds (I) having the amino acid sequences of SEQ ID NO:3, 5 and 7
 CC (ADR29359, ADR29361 and ADR29363). Also described: (1) a peptide (II)
 CC comprising the 3011 amino acid sequence of SEQ ID NO:1 (SI. ADR29357),
 CC where in (SI) positions 2594-2602 are Phe, Ile, Leu, Trp, Pro, Glu, Asn,
 CC Lys, and Val (SEQ ID NO:3), respectively or Phe, Leu, Pro, Trp, Gly, Ala,
 CC Trp, Lys, and Val (SEQ ID NO:5) respectively; (2) a polynucleotide (III)
 CC that encodes Phe-Leu-Ile-Trp-Pro-Glu-Asn-Lys-Val; Phe-Leu-Pro-Trp-Gly-Ala
 CC -Trp-Lys-Val, or Ala-Leu-Tyr-Asp-Val-Thr-Lys-Leu (SEQ ID NO:3, 5 or 7);
 CC (3) an antibody (IV) that recognises and binds to (I); (4) an immune
 CC effector cell (V) that has been raised in vivo or in vitro or in the
 CC presence and the expense of an antigen presenting cell that presents (I),
 CC in the context of an MHC molecule; (5) a composition (VI) comprising (I)
 CC of SEQ ID NO:3, 5 or 7 where (I) is individually characterised by an
 CC ability to elicit an immune response against the same native ligand; (6)
 CC a composition (VII) comprising (I) and a carrier; (7) a host cell (VIII)
 CC comprising at least one or more (I) of SEQ ID NO:3, 5 or 7 that are
 CC individually characterised by an ability to elicit an immune response
 CC against the same native ligand; and (8) a composition comprising (VIII)
 CC and a carrier. (I) have anti-HIV, virucide, antiinflammatory,
 CC hepatotropic and immunostimulant activities, and can be used in vaccines.
 CC (I) can be used for inducing an immune response in a subject which
 CC involves delivering (I) to the subject. (I) is delivered in the context
 CC of an MHC molecule. The MHC molecules presents (I) on the surface of an
 CC antigen presenting cell. (I) is delivered as a polynucleotide that
 CC encodes it. (IV) is useful for immunotherapy. (V) is useful for adoptive
 CC immunotherapy. (VI) is useful for inducing an immune response in a
 CC subject. (I) is useful as components of anti-HCV vaccines and to expand
 CC immune effector cell that are specific for cells expressing HCV epitope.
 CC (I) is useful for preparation of medicament for diagnosis and treatment
 CC of diseases such as AIDS. The present sequence represents the hepatitis C
 CC virus polyprotein precursor, which is used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 3011 AA;
 Query Match 99.5%; Score 1035; DB 8; Length 3011;
 Best Local Similarity 99.5%; Pred. No. 1.9e-89;
 Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSTNPKQKKKNTNRPPQDVKFGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
 DB 1 MSTNPKQKKKNTNRPPQDVKFGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
 QY 61 RRQPIPKARRPEGRRTWAQPGYPMWLYGNECGWAGLLSPRGSPPSGWPTDPRRRSRNLG 120
 DB 61 RRQPIPKARRPEGRRTWAQPGYPMWLYGNECGWAGLLSPRGSPPSGWPTDPRRRSRNLG 120
 QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAAARALAHGVRVLEDGVNATGNLPGCSFSIFLLA 180
 DB 121 KVIDTLTCGFADLMGYIPVGLGAPLGGAAARALAHGVRVLEDGVNATGNLPGCSFSIFLLA 180
 QY 181 LLSCLTVPAS 190
 DB 181 LLSCLTVPAS 190

QY 181 LLSCLTVPAS 191
 DB 181 LLSCLTVPAS 191
 RESULT 13
 ADE39661
 ID ADE39661 standard; protein; 190 AA.
 XX ADE39661;
 AC ADE39661;
 XX 29-JAN-2004 (first entry)
 DT Hepatitis C virus core protein full-length amino acid sequence.
 XX Hepatitis C virus; HCV; HCV core protein; hepatitis C virus core protein;
 KW transfusion-associated hepatitis; community-acquired hepatitis;
 KW hepatitis; core antigen; anti-core antibody; HCV infection.
 XX Hepatitis C virus.
 OS
 XX EPI310796-A2.
 PN 14-MAY-2003.
 XX 05-NOV-2002; 2002EP-00257659.
 PF 07-NOV-2001; 2001US-0347943P.
 PR 10-OCT-2002; 2002US-00268562.
 XX (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
 PA Bahl C;
 PI WPI; 2003-543593/52.
 XX Antibody/antigen composition useful for detecting hepatitis C virus,
 CC comprises mixture of hepatitis C virus protein, modified hepatitis C
 CC virus core protein and anti-core antibodies.
 Example 3; SEQ ID NO 1; 8pp; English.
 This invention relates to a novel antibody/antigen composition which
 CC comprises a mixture of hepatitis C virus (HCV) protein and modified HCV
 CC core protein and anti-core antibodies that do not recognise HCV core
 CC amino acids 10-43. HCV is a leading cause of transfusion-associated and
 CC community-acquired hepatitis. The invention is useful in an immunoassay
 CC for HCV or for detecting core antigen and anti-core antibodies in serum
 CC collected from HCV infected individuals. The present sequence is that of
 CC the full-length hepatitis C virus (HCV) core protein which was used
 CC during the creation of the composition of the invention.
 XX Sequence 190 AA;
 Query Match 99.1%; Score 1031; DB 7; Length 190;
 Best Local Similarity 99.5%; Pred. No. 1.9e-90;
 Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSTNPKQKKKNTNRPPQDVKFGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
 DB 1 MSTNPKQKKKNTNRPPQDVKFGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
 QY 61 RRQPIPKARRPEGRRTWAQPGYPMWLYGNECGWAGLLSPRGSPPSGWPTDPRRRSRNLG 120
 DB 61 RRQPIPKARRPEGRRTWAQPGYPMWLYGNECGWAGLLSPRGSPPSGWPTDPRRRSRNLG 120
 QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAAARALAHGVRVLEDGVNATGNLPGCSFSIFLLA 180
 DB 121 KVIDTLTCGFADLMGYIPVGLGAPLGGAAARALAHGVRVLEDGVNATGNLPGCSFSIFLLA 180
 QY 181 LLSCLTVPAS 190
 DB 181 LLSCLTVPAS 190

```
Db      181 LLSCLTVPAS 190

RESULT 14
AAR14557
ID AAR14557 standard; protein; 215 AA.
XX
XX AAR14557;
AC
XX
XX 24-OCT-2003 (revised)
DT 24-JAN-1992 (first entry)
XX
XX HCV Capsid protein encoded by clone 56.
DE
XX non-A, non-B hepatitis; PT-NANBH; liver disease.
KW
XX Hepatitis C virus; Virus.
OS
XX WO9115516-A.
PN
XX 17-OCT-1991.
PD
XX
XX 06-APR-1990; 90US-00505611.
PF
XX
XX 06-APR-1990; 90US-00505611.
PR
XX 09-OCT-1990; 90US-00594854.
PR
XX (GENE-) GENELABS INC.
PA
XX
XX Reyes G, Kim JP, Moeckli R, Simonsen CC;
PI
XX WPI; 1991-325174/44.
DR
XX N-PSDB; AAQ14279.
DR
XX
XX Hepatitis C virus epitope(s) immuno-reactive with HCV infected sera
PT - useful for detection of HCV infections and as HCV vaccine.
PT
XX
XX Claim 14; Page 110; 150pp; English.
PS
XX Putative HCV capsid protein clones were identified by immunoscreening.
CC Clone 56 was sequenced and found to include a run of adenine residues
CC around nucleotides 25 to 34; such sequences are similar to sequences
CC known to promote translation frameshifting. The mol. wt. of the protein
CC deduced from the open reading frame is 23.5kd. (Updated on 24-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 215 AA;

Query Match      99.1%; Score 1031; DB 2; Length 215;
Best Local Similarity 99.0%; Pred. No. 2.2e-90;
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNKNTNRRPDQVFPGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 60
Db 1 MGTNPKQKKNKNTNRRPDQVFPGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 60
QY 61 RRQPIKARRPEGRRTWAQPGYPWPPLYGNECCGAGWLLSPRGRSPSWGPTDPRRSRNLG 120
Db 61 RRQPIKARRPEGRRTWAQPGYPWPPLYGNECCGAGWLLSPRGRSPSWGPTDPRRSRNLG 120
QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPVLPVAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

Search completed: August 19, 2005, 12:39:27
Job time : 119.5 secs
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```
AC AAR14558;
XX
XX 24-OCT-2003 (revised)
DT 24-JAN-1992 (first entry)
XX
XX Polypeptide encoded by modified HCV Capsid protein clone pGEX-CapA.
DE
XX non-A, non-B hepatitis; PT-NANBH; liver disease.
KW
XX Hepatitis C virus; Virus.
OS
XX WO9115516-A.
PN
XX 17-OCT-1991.
PD
XX
XX 06-APR-1990; 90US-00505611.
PF
XX
XX 06-APR-1990; 90US-00505611.
PR
XX 09-OCT-1990; 90US-00594854.
PR
XX (GENE-) GENELABS INC.
PA
XX
XX Reyes G, Kim JP, Moeckli R, Simonsen CC;
PI
XX WPI; 1991-325174/44.
DR
XX N-PSDB; AAQ14280.
DR
XX
XX Hepatitis C virus epitope(s) immuno-reactive with HCV infected sera
PT - useful for detection of HCV infections and as HCV vaccine.
PT
XX
XX Claim 14; Fig 8B; 150pp; English.
PS
XX Putative HCV capsid protein clones were identified by immunoscreening.
CC Clone 56 was sequenced and found to include a run of adenine residues
CC around nucleotides 25 to 34; such sequences are similar to sequences
CC known to promote translation frameshifting. To improve expression of the
CC HCV capsid protein the putative region of frameshifting was modified
CC (i.e. adenine residues at the third position of a codon were changed to
CC guanines) to give pGEX-CapA. See AAQ14279 for the unmodified clone 56
CC sequence. (Updated on 24-OCT-2003 to standardise OS field)
XX
XX Sequence 215 AA;

Query Match      99.1%; Score 1031; DB 2; Length 215;
Best Local Similarity 99.0%; Pred. No. 2.2e-90;
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSTNPKQKKNKNTNRRPDQVFPGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 60
Db 1 MGTNPKQKKNKNTNRRPDQVFPGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRG 60
QY 61 RRQPIKARRPEGRRTWAQPGYPWPPLYGNECCGAGWLLSPRGRSPSWGPTDPRRSRNLG 120
Db 61 RRQPIKARRPEGRRTWAQPGYPWPPLYGNECCGAGWLLSPRGRSPSWGPTDPRRSRNLG 120
QY 121 KVIDTLTCGFADLMGYIPAVGAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
Db 121 KVIDTLTCGFADLMGYIPVLPVAPLGGAARALAHGVRLVDGVNYATGNLPGCSFSIFLLA 180
QY 181 LLSCLTVPASA 191
Db 181 LLSCLTVPASA 191

Search completed: August 19, 2005, 12:39:27
Job time : 119.5 secs
```

```
Db      181 LLSCLTVPAS 190

RESULT 15
AAR14558
ID AAR14558 standard; protein; 215 AA.
XX
XX
```


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OM protein - protein search, using sw model

Run on: August 23, 2005, 13:22:28 ; Search time 165 Seconds
(without alignments)

27.932 Million cell updates/sec

Title: US-10-770-117-1

Perfect score: 47

Sequence: 1 DLMGYIPAV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 68540

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	59.6	50	2	Q9C1W4
2	27	57.4	27	2	Q66269
3	27	57.4	27	2	Q66270
4	27	57.4	32	2	Q89492
5	27	57.4	46	2	Q8WTQ2
6	27	57.4	48	2	Q9P4B0
7	27	57.4	16	2	Q8R963
8	26	55.3	19	2	Q9UCH5
9	26	55.3	24	2	Q94370
10	26	55.3	38	2	Q8EG71
11	26	55.3	40	2	Q9PA42
12	26	55.3	41	2	Q663D0
13	26	55.3	44	2	Q9QZ58
14	26	55.3	44	2	Q9ZG06
15	26	55.3	46	2	Q9WP35
16	26	55.3	50	2	Q6AIU2
17	26	55.3	50	2	Q84859
18	25	53.2	21	2	Q7M035
19	25	53.2	24	2	Q7M1L8
20	25	53.2	27	1	PSAF_SYNVU
21	25	53.2	31	2	Q8Z612
22	25	53.2	32	2	Q8ES42
23	25	53.2	36	2	Q8G5S5
24	25	53.2	39	2	Q8G6I9
25	25	53.2	39	2	Q8G6J0
26	25	53.2	39	2	Q8G6J1
27	25	53.2	39	2	Q8G6J2
28	25	53.2	39	2	Q8G6J3
29	25	53.2	39	2	Q8G6J4
30	25	53.2	39	2	Q8G6J5
31	25	53.2	39	2	Q8G6J6

32	25	53.2	39	2	Q866J6
33	25	53.2	39	2	Q866J7
34	25	53.2	39	2	Q866J8
35	25	53.2	39	2	Q866J9
36	25	53.2	39	2	Q866K0
37	25	53.2	39	2	Q866K1
38	25	53.2	39	2	Q866K2
39	25	53.2	39	2	Q866K3
40	25	53.2	40	2	Q91K22
41	25	53.2	43	2	Q72BP3
42	25	53.2	44	1	N160_XENLA
43	25	53.2	47	2	Q7UYN7
44	25	53.2	49	1	Y16H_BPT4
45	25	53.2	49	2	Q64CG7
46	24.5	52.1	47	2	Q9CW87
47	24	51.1	18	2	Q6LD16
48	24	51.1	25	2	Q9BG19
49	24	51.1	25	2	Q9WMI4
50	24	51.1	27	2	Q9TZ20
51	24	51.1	29	2	Q93DQ1
52	24	51.1	33	2	Q6UAS5
53	24	51.1	36	1	NLTP_PINPI
54	24	51.1	36	1	PSAL_CVACA
55	24	51.1	36	2	Q8CTU7
56	24	51.1	36	2	Q35355
57	24	51.1	38	2	Q886X3
58	24	51.1	40	2	Q879L6
59	24	51.1	42	2	Q7MRD6
60	24	51.1	45	2	Q8PF22
61	24	51.1	46	2	Q8EHZ6
62	24	51.1	47	2	Q86UL5
63	24	51.1	49	2	Q6EEJ0
64	24	51.1	49	2	Q9S0U2
65	23	48.9	9	2	Q88612
66	23	48.9	12	1	RF1_CONSP
67	23	48.9	16	2	Q7M263
68	23	48.9	18	2	Q9S8Y9
69	23	48.9	20	2	Q7M262
70	23	48.9	20	2	Q7M264
71	23	48.9	20	2	Q9S8X9
72	23	48.9	20	2	Q9S8Y0
73	23	48.9	23	2	Q6JDN4
74	23	48.9	25	2	Q8LTE8
75	23	48.9	25	2	Q7PCD2
76	23	48.9	30	2	Q9TQ11
77	23	48.9	31	2	Q9QYV4
78	23	48.9	33	2	Q15747
79	23	48.9	33	2	Q9KSG4
80	23	48.9	34	2	Q13871
81	23	48.9	34	2	Q9RCC0
82	23	48.9	34	2	Q9RCD1
83	23	48.9	34	2	Q8F1R4
84	23	48.9	34	2	Q9W7P6
85	23	48.9	35	2	Q7M3X7
86	23	48.9	35	2	Q18877
87	23	48.9	35	2	Q9TSX6
88	23	48.9	35	2	Q7TTL5
89	23	48.9	35	2	Q7TTL7
90	23	48.9	35	2	Q9YNI2
91	23	48.9	36	2	Q7QV88
92	23	48.9	36	2	Q9NGN1
93	23	48.9	37	2	Q8EDY3
94	23	48.9	38	2	Q7M0Q2
95	23	48.9	38	2	Q9JUP1
96	23	48.9	43	2	Q722M6
97	23	48.9	44	2	Q83YL2
98	23	48.9	44	2	Q9REI7
99	23	48.9	44	2	Q7V203
100	23	48.9	45	2	Q84WH1

ALIGNMENTS

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RESULT 1
ID Q9C1W4 PRELIMINARY; PRT; 50 AA.
AC Q9C1W4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SPBC713.11c protein.
GN Name=SPBC713.11c;
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Gobie A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jägers K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares K., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S.,
RA Gabel C., Fuchs M., Dusterhoft A., Fritz C., Holzer E., Moestl D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Leirach H., Reinhardt R.,
RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle S.,
RA Goffeau A., Cadieu E., Drano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dega R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
DR EMBL; AL512943; CAC22612.1; -.
DR GeneDB SPombe; SPBC713.11c; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000612; UPF0057.
DR Pfam; PF01679; UPF0057; 1.
DR PROSITE; PS01309; UPF0057; 1.
SQ SEQUENCE 50 AA; 5475 MW; 503B8FEFC027EF2 CRC64;

Query Match 59.6%; Score 28; DB 2; Length 50;
Best Local Similarity 42.9%; Pred. No. 8.6e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 MGYPAP 9
Db 34 LGYVPGI 40

RESULT 2
Q66269 PRELIMINARY; PRT; 27 AA.
AC Q66269;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cucurbit mosaic virus open reading frame, complete cds, and satellite RNA.
OS Cucurbit mosaic virus (cucurbit mosaic cucumovirus).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;

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OC Cucumovirus.
OX NCBI_TaxID=12305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F;
RX MEDLINE=90171930; PubMed=1689769;
RA Hidaka S., Hanada K., Ishikawa K.;
RT "In vitro messenger properties of a satellite RNA of cucumber mosaic virus."
RL J. Gen. Virol. 71:439-442(1990).
DR EMBL; D00699; BAA00605.1; -.
SQ SEQUENCE 27 AA; 2874 MW; 1DDA41BF3FAL328A CRC64;

Query Match 57.4%; Score 27; DB 2; Length 27;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MGYPAP 8
Db 19 VGYLPA 24

RESULT 3
Q66270 PRELIMINARY; PRT; 27 AA.
AC Q66270;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Cucurbit mosaic virus (cucurbit mosaic cucumovirus).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OX NCBI_TaxID=12305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E;
RX MEDLINE=88219519; PubMed=3369085;
RA Hidaka S., Hanada K., Ishikawa K., Miura K.;
RT "Complete nucleotide sequence of two new satellite RNAs associated with cucumber mosaic virus."
RL Virology 164:326-333(1988).
DR EMBL; M20844; AAA66611.1; -.
KW Hypothetical protein.
SQ SEQUENCE 27 AA; 2783 MW; 1D80426D890A462F CRC64;

Query Match 57.4%; Score 27; DB 2; Length 27;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MGYPAP 8
Db 19 VGYLPA 24

RESULT 4
Q89492 PRELIMINARY; PRT; 27 AA.
AC Q89492;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ORF 1.
OS Cucurbit mosaic virus (cucurbit mosaic cucumovirus).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OX NCBI_TaxID=12305;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88179532; PubMed=3354198;
RA Kaper J.M., Tounignant M.E., Steen M.T.;
RT "Cucurbit mosaic virus-associated RNA 5: XI. Comparison of 14 CARNA 5 variants relates ability to induce tomato necrosis to a conserved

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RT nucleotide sequence."
RL Virology 163:284-292(1988).
DR EMBL; M20357; AAA46403.1; -.
DR EMBL; M20350; AAA46385.1; -.
DR EMBL; M20352; AAA46388.1; -.
DR EMBL; M20353; AAA46391.1; -.
DR EMBL; M20354; AAA46394.1; -.
DR EMBL; M20355; AAA46397.1; -.
DR EMBL; M20356; AAA46400.1; -.
DR PIR; JE0015; JE0015.
DR PIR; JS0104; JS0104.
SQ SEQUENCE 27 AA; 2827 MW; BC60426D890A5B9A CRC64;

Query Match 57.4%; Score 27; DB 2; Length 27;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 MGYIPA 8
Db 19 VGYLPA 24

RESULT 5
Q7KYP7 PRELIMINARY; PRT; 32 AA.
AC Q7KYP7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Dystrophin C-terminal region (32 AA) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=8181947; PubMed=2648158; DOI=10.1038/338509a0;
RA Feener C.A., Koenig M., Kunkel L.M.;
RT "Alternative splicing of human dystrophin mRNA generates isoforms at
the carboxy terminus.";
RL Nature 338:509-511(1989).
DR EMBL; X15149; CAA33246.1; -.
FT NON_TER 1
SQ SEQUENCE 32 AA; 3856 MW; CC3917998F22F47E CRC64;

Query Match 57.4%; Score 27; DB 2; Length 32;
Best Local Similarity 80.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 MGYIP 7
Db 16 MGYLP 20

RESULT 6
Q8WTQ2 PRELIMINARY; PRT; 46 AA.
AC Q8WTQ2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Dystrophin (Fragment).
GN Name=DMD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Beggs A.H., Koenig M., Kunkel L.M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]

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RP SEQUENCE FROM N.A.
RA den Dunnen J.T.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF213442; AAL61586.1; -.
DR EMBL; AF213442; AAL61587.1; -.
FT NON_TER 1
FT NON_TER 46
SQ SEQUENCE 46 AA; 5376 MW; DE4AC42C16208108 CRC64;

Query Match 57.4%; Score 27; DB 2; Length 46;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 MGYIP 7
Db 30 MGYLP 34

RESULT 7
Q9P4B0 PRELIMINARY; PRT; 48 AA.
AC Q9P4B0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Letharia vulpina.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
OC Lecanorales; Lecanorineae; Parmeliaceae; Letharia.
OX NCBI_TaxID=129387;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21546980; PubMed=11686674; DOI=10.1006/fghi.2001.1291;
RA Kroken S., Taylor J.W.;
RT "Outcrossing and recombination in the lichenized fungus Letharia.";
RL Fungal Genet. Biol. 34:83-92(2001).
DR EMBL; AF228463; AAF87290.1; -.
KW Hypothetical protein.
FT NON_TER 48
SQ SEQUENCE 48 AA; 5779 MW; 9APE570D10BF9755 CRC64;

Query Match 57.4%; Score 27; DB 2; Length 48;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LMGYIP 7
Db 27 LKGYIP 32

RESULT 8
Q9R963 PRELIMINARY; PRT; 16 AA.
AC Q9R963;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE PepC (Fragment).
GN Name=pepC;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F31;
RX MEDLINE=98453456; PubMed=9780260;
RA Ito Y., Azuma T., Ito S., Suto H., Miyaji H., Yamazaki Y., Kohli Y.,
RA Kuriyama M.;
RT "Full-length sequence analysis of the vacA gene from cytotoxic and
noncytotoxic Helicobacter pylori.";
RL Infect. Dis. 178:1391-1398(1998).
DR EMBL; AF049623; AAD04263.1; -.

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FT  NON TER      1      1
FT  NON_TER     16     16
SQ  SEQUENCE    16 AA; 1938 MW;  3C33D403ABE61428 CRC64;

Query Match      55.3%; Score 26; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy  2  LMGYIPAV 9
    | : || |
Db  1  LIAYIPQV 8

RESULT 9
Q9UCH5 Q9UCH5 PRELIMINARY; PRT; 19 AA.
AC Q9UCH5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Natural killer enhancing factor, NKEF (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93215001; PubMed=8462106; DOI=10.1006/cimm.1993.1043;
RA Shau H., Gupta R.K., Golub S.H.;
RT "Identification of a natural killer enhancing factor (NKEF) from human
RT erythroid cells.";
RL Cell. Immunol. 147:1-11(1993).
DR GO; GO:0005829; C:cytosol; NAS.
FT  NON TER      1
FT  NON_TER     19
SQ  SEQUENCE    19 AA; 2012 MW;  69DC04F5DD5BC56F CRC64;

Query Match      55.3%; Score 26; DB 2; Length 19;
Best Local Similarity 62.5%; Pred. No. 9.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy  1  DLMGYIPA 8
    | : || |
Db  9  DEMGEVPA 16

RESULT 10
Q94370 Q94370 PRELIMINARY; PRT; 24 AA.
AC Q94370;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PPI-like Ser/Thr protein phosphatase (fragment).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodirinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeke T., Gergely P., Dombradi V.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBSJ databases.
DR EMBL; 277730; CAB01289.1; -.
DR PIR; T42390; T42390.
FT  NON TER      1
FT  NON_TER     24
SQ  SEQUENCE    24 AA; 2787 MW;  004023AE033FCD01 CRC64;

Query Match      55.3%; Score 26; DB 2; Length 24;
Best Local Similarity 55.6%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy  1  DLMGYIPAV 9
    | : || |

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Db  10  DAVGYPPKV 18
    | : || |

RESULT 11
Q8EG71 Q8EG71 PRELIMINARY; PRT; 38 AA.
AC Q8EG71;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SO1737.
GN OrderedLocusNames=SO1737;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA White O., Wolf A.M., Vamathevan J.U., Weidman J.F., Imbraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Nealon K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AE015618; AAN54791.1; -.
DR TIGR; SO1737; -.
KW Complete proteome; Hypothetical protein.
SQ  SEQUENCE    38 AA; 4405 MW;  410074CB8F607359 CRC64;

Query Match      55.3%; Score 26; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2  LMGYI 6
    | : || |
Db  5  LMGYI 9

RESULT 12
Q9PA42 Q9PA42 PRELIMINARY; PRT; 40 AA.
AC Q9PA42;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=Xf2678;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5c;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.B., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

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RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuranae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado A.M., Madeira A.M.B.N., Martins E.M.F., Marino C.L.,
RA Marques M.V., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Menck C.F.M., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nogueira F.G., Nunes L.R., Oliveira M.A.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Palmieri D.A., Paris A.,
RA de Oliveira M.C., de Oliveira R.C., Rodrigues V., de Rosa A.J.M.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa."
RL Nature 406:151-159(2000).
DR EMBL: AE004073; AAF85475.1; -.
DR PIR: A82529; A82529.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 40 AA; 4601 MW; 4C42AF68E5999933 CRC64;

Query Match 55.3%; Score 26; DB 2; Length 40;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LMGYIPAV 9
Db 3 LLGYVESV 10

RESULT 13
Q663D0 PRELIMINARY; PRT; 41 AA.
AC Q663D0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=pYtb0024;
OS Yersinia pseudotuberculosis IP 32953.
OG Plasmid pYtb32953.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=273123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP 32953;
RX PubMed=15358858;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
RA Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the genome evolution of Yersinia pestis through whole
RT genome comparison with Yersinia pseudotuberculosis."
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
DR EMBL: BX936400; CAF25466.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 41 AA; 4704 MW; 89DC6E905AE923F0 CRC64;

Query Match 55.3%; Score 26; DB 2; Length 41;
Best Local Similarity 71.4%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIP 7
Db 15 NLGGYIP 21

RESULT 14

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Q7QZ58 PRELIMINARY; PRT; 44 AA.
AC Q7QZ58;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GUP_22_47461_47327.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB CG;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AACB0100045; EAA40351.1; -.
SQ SEQUENCE 44 AA; 5425 MW; 6CCAB8846627693A CRC64;

Query Match 55.3%; Score 26; DB 2; Length 44;
Best Local Similarity 71.4%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 MGYIPAV 9
Db 1 MGLIPSV 7

RESULT 15
Q9ZGU6 PRELIMINARY; PRT; 44 AA.
AC Q9ZGU6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Regulatory protein.
GN OrderedLocNames=L7024;
OS Escherichia coli O157:H7.
OC Plasmid pO157.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=98391744; PubMed=9722640; DOI=10.1093/nar/26.18.4196;
RA Burland V., Shao Y., Perna N.T., Plunkett G. III, Sofia H.J.,
RA Blattner F.R.;
RT "The complete DNA sequence and analysis of the large virulence plasmid
RT of Escherichia coli O157:H7."
RL Nucleic Acids Res. 26:4196-4204 (1998).
DR EMBL: AF074613; AAC70092.1; -.
DR PIR: T42124; T42124.
DR InterPro; IPR011010; DNA_brk_join_enz.
KW Complete proteome; Plasmid.
SQ SEQUENCE 44 AA; 4951 MW; 824EF81ED8273816 CRC64;

Query Match 55.3%; Score 26; DB 2; Length 44;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LMGYIPAV 9
Db 12 LMGYLHGV 19

RESULT 16
Q9WP35 PRELIMINARY; PRT; 46 AA.
ID Q9WP35

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AC Q9WP35;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative core/capsid protein (Fragment).
OS TT virus.
OC Viruses; ssDNA viruses; Anellovirus.
OX NCBI_TaxID=69887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93350008; PubMed=10423145;
RA Ball J K., Curran R., Berridge S., Grabowska A.M., Jameson C.L.,
RA Thomson B.J., Irving W.L., Sharp P.M.;
RT "TT virus sequence heterogeneity in vivo: evidence for co-infection
RT with multiple genetic types.";
RL J. Gen. Virol. 80:1759-1768(1999).
DR EMBL; AF145015; AAD42373.1; -.
DR InterPro; IPR004219; TTvirus_Unk.
DR Pfam; PF02956; TT_ORF1.1.
FT NON_TER 1
FT TER 46
SQ SEQUENCE 46 AA; 5256 MW; 335B2E92048DFEC3 CRC64;
Query Match 55.3%; Score 26; DB 2; Length 46;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 LMGYIP 7
Db 35 LRGYVP 40
RESULT 17
Q6AIU2
ID Q6AIU2 PRELIMINARY; PRT; 50 AA.
AC Q6AIU2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein.
GN OrderedLocusNames=DP3009;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
OC Desulfobulbaceae; Desulfotalea.
OX NCBI_TaxID=84980;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=LSv54 / DSM 12343;
RX PubMed=15305914;
RA Rabus R., Ruepp A., Frickey T., Rattei T., Partmann B., Stark M.,
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
RA Klenk H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
RT from permanently cold Arctic sediments.";
RL Environ. Microbiol. 6:887-902(2004).
DR EMBL; CR522870; CAG37738.1; -.
KW Complete proteome.
SQ SEQUENCE 50 AA; 5611 MW; 0882A7347C205CD4 CRC64;
Query Match 55.3%; Score 26; DB 2; Length 50;
Best Local Similarity 62.5%; Pred. No. 2.2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DLMGYIPA 8
Db 39 DLPGYNPS 46
RESULT 18
Q84859
ID Q84859 PRELIMINARY; PRT; 19 AA.
AC Q84859;
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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Unidentified human poliovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=40278;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87169734; PubMed=3031313;
RA Kuge S., Saito I., Nomoto A.;
RT "Primary structure of poliovirus defective-interfering particle
RT genomes and possible generation mechanisms of the particles.";
RL J. Mol. Biol. 192:473-487(1986).
DR EMBL; M30216; AAA66825.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT TER 19
SQ SEQUENCE 19 AA; 2127 MW; F4D2596021AAEA1A CRC64;
Query Match 53.2%; Score 25; DB 2; Length 19;
Best Local Similarity 37.5%; Pred. No. 1.4e+03;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DLMGYIPA 8
Db 12 DILGFVSA 19
RESULT 19
Q7M035
ID Q7M035 PRELIMINARY; PRT; 21 AA.
AC Q7M035;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Protein kinase.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RX MEDLINE=933737942; PubMed=8365414;
RA Brunati A.M., James P., Donella-Deana A., Matoskova B., Robbins K.C.,
RA Pinna L.A.;
RT "Isolation and identification of two proto-oncogene products related
RT to c-fgr and fyn in a tyrosine-protein-kinase fraction of rat
RT spleen.";
RL Eur. J. Biochem. 216:323-327(1993).
DR PIR; S35676; S35676.
DR HSSP; P06241; IG83.
DR InterPro; IPR001452; SH3.
DR ProDom; PD000066; SH3.1.
SQ SEQUENCE 21 AA; 2335 MW; 40213D1508152FF8 CRC64;
Query Match 53.2%; Score 25; DB 2; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GYIPA 8
Db 15 GXIPS 19
RESULT 20
Q7M1L8
ID Q7M1L8 PRELIMINARY; PRT; 24 AA.
AC Q7M1L8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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DE Pollen allergen Phl p V (Fragment).
OS Phleum pratense (Common timothy).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poales; Poaceae; Pooidae;
OC Avenae; Phleum.
OX NCBI_TaxID=15957;
RN [1]
RP SEQUENCE
RX MEDLINE=91322736; PubMed=1863892;
RA Matthies F., Lowenstein H.;
RT "Group V allergens in grass pollens. I. Purification and
RT characterization of the group V allergen from Phleum pratense pollen,
RT Phl p V.";
RL Clin. Exp. Allergy 21:297-307(1991).
DR PIR; A61505; A61505. 1
FT NON TER 24 24
FT NON TER 24 24
SQ SEQUENCE 24 AA; 2198 MW; 6232BAF9CC85C17A CRC64;

Query Match 53.2%; Score 25; DB 2; Length 24;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 MGYIPA 8
Db 2 LGYAPA 7

RESULT 21
PSAF SYNNU STANDARD; PRT; 27 AA.
AC P23076;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Photosystem I reaction centre subunit III (PSI-F) (Fragment).
GN Name=psaf;
OS Synecococcus vulcanus (Thermosynechococcus vulcanus).
OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
OX NCBI_TaxID=32053;
RN [1]
RP SEQUENCE.
RX MEDLINE=89338747; PubMed=2503399; DOI=10.1016/0014-5793(89)80971-8;
RA Koike H., Ikeuchi M., Hiyama T., Inoue Y.;
RT "Identification of photosystem I components from the cyanobacterium,
RT Synecococcus vulcanus by N-terminal sequencing.";
RL FEBS Lett. 253:257-263(1989).
CC -I- FUNCTION: Probably participates in efficiency of electron transfer
CC from plastocyanin to P700 (or cytochrome c553 in algae and
CC cyanobacteria). This plastocyanin-docking protein contributes to
CC the specific association of plastocyanin to PSI.
CC -I- SIMILARITY: Belongs to the psaf family.
DR InterPro; IPR003666; PSI_Psaf.
DR Pfam; PF02507; PSI_Psaf.1.
KW Direct protein sequencing; Photosynthesis; Photosystem I.
FT NON TER 27 27
FT NON TER 27 27
SQ SEQUENCE 27 AA; 2685 MW; 30FFACDC3F258CM4 CRC64;

Query Match 53.2%; Score 25; DB 1; Length 27;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DLMGYIPA 8
Db 1 DVAGLVPA 8

RESULT 22
Q8Z612 PRELIMINARY; PRT; 31 AA.
AC Q8Z612;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein STV2049.
GN OrderedLocusNames=STV2049;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.R.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL627272; CAD05592.1; --
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 31 AA; 3168 MW; E3B537F92EE34199 CRC64;

Query Match 53.2%; Score 25; DB 2; Length 31;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LMGYIP 7
Db 7 IRGYIP 12

RESULT 23
Q9ES42 PRELIMINARY; PRT; 32 AA.
AC Q9ES42;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Thyroid hormone receptor beta 3 (Fragment).
GN Name=TRbeta;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
RX MEDLINE=20501244; PubMed=11046130;
RX DOI=10.1128/MCB.20.22.8329-8342.2000;
RA Williams G.R.;
RT "Cloning and characterization of two novel thyroid hormone receptor
RT beta isoforms.";
RL Mol. Cell. Biol. 20:8329-8342(2000).
DR EMBL; AF239915; AAC33351.1; --
DR GO; GO:0004872; F:receptor activity; IEA.
KW NON TER 32 32
KW NON TER 32 32
SQ SEQUENCE 32 AA; 3696 MW; BA134847AC9B5F42 CRC64;

Query Match 53.2%; Score 25; DB 2; Length 32;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GYIPA 8
Db 24 GYIP 28

RESULT 24

DR	HSP; P00747; IKI0.
DR	InterPro; IPR000001; Kringle.
DR	Pfam; PF00051; Kringle; 1.
DR	PRINTS; PR00018; KRINGLE.
DR	PROSITE; PS00070; KRINGLE_2; 1.
KW	Kringle.
FT	NON_TER 1
FT	NON_TER 39 39
FT	NON_TER 39 39
SEQ	SEQUENCE 39 AA; 4300 MW; A8DD66BB44393F02 CRC64;
 Query Match 53.2%; Score 25; DB 2; Length 39; Best Local Similarity 80.0%; Pred.No. 2.7e+03; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	4 GYIPA 8
Db	:
	35 GYIPS 39
 RESULT 26 Q866J0 PRELIMINARY; PRT; 39 AA. ID Q866J0 AC Q866J0 DT 01-JUN-2003 (TREMBLrel. 24, Created) DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update) DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update) DE Plasminogen (Fragment). GN Name=PLG; OS Miopithecus talapoin (Talapoin) (Cercopithecus talapoin). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; OC Cercopitheciinae; Miopithecus. OX NCBI_TaxID=36231; RN [1] RP SEQUENCE FROM N.A. RA Boffelli D., Lewis K.D., Rubin E.M.; RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. DR EMBL; AV192767; AAC19634.1; -. DR HSP; P00747; IKI0. DR InterPro; IPR000001; Kringle. DR Pfam; PF00051; Kringle; 1. DR PROSITE; PS00070; KRINGLE_2; 1. KW Kringle. FT NON_TER 1 FT NON_TER 39 39 FT NON_TER 39 39 SEQ SEQUENCE 39 AA; 4286 MW; A8DBBDBB44393F02 CRC64;	
 Query Match 53.2%; Score 25; DB 2; Length 39; Best Local Similarity 80.0%; Pred.No. 2.7e+03; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	4 GYIPA 8
Db	:
	35 GYIPS 39
 RESULT 27 Q866J1 PRELIMINARY; PRT; 39 AA. ID Q866J1 AC Q866J1 DT 01-JUN-2003 (TREMBLrel. 24, Created) DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update) DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update) DE Plasminogen (Fragment). GN Name=PLG; OS Ateles Geoffroyi (Black-handed spider monkey). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleae. OX NCBI_TaxID=9509; RN [1] RP SEQUENCE FROM N.A. RA Boffelli D., Lewis K.D., Rubin E.M.; RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.	


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DR EMBL; AY192766; AAO19633.1; -.
DR HSSP; P00747; IK10.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 1.
DR PRINTS; PR00018; KRINGLE.
DR PROSITE; PS50070; KRINGLE_2; 1.
DR KRINGLE.
KW Kringle.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4328 MW; 595466BB44393F10 CRC64;

Query Match 53.2%; Score 25; DB 2; Length 39;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYIPA 8
DB 35 GYIPS 39

RESULT 28
Q866J2 ID Q866J2 PRELIMINARY; PRT; 39 AA.
AC Q866J2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Plasminogen (Fragment).
GN Name=PLG;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Boffelli D., Lewis K.D., Rubin E.M.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY192765; AAO19632.1; -.
DR HSSP; P00747; IK10.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 1.
DR PROSITE; PS50070; KRINGLE_2; 1.
DR KRINGLE.
KW Kringle.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4286 MW; A8DBBDBB44393F02 CRC64;

Query Match 53.2%; Score 25; DB 2; Length 39;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYIPA 8
DB 35 GYIPS 39

RESULT 29
Q866J3 ID Q866J3 PRELIMINARY; PRT; 39 AA.
AC Q866J3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Plasminogen (Fragment).
GN Name=PLG;
OS Nasalis larvatus (Proboscis monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae; Colobinae;
OC Nasalis.
OX NCBI_TaxID=43780;
RN [1]
RP SEQUENCE FROM N.A.

RA Boffelli D., Lewis K.D., Rubin E.M.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY192763; AAO19630.1; -.
DR HSSP; P00747; IK10.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS50070; KRINGLE_2; 1.
DR KRINGLE.
KW Kringle.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4242 MW; A8DD66BB47090C02 CRC64;

Query Match 53.2%; Score 25; DB 2; Length 39;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYIPA 8
DB 35 GYIPS 39

RESULT 30
Q866J4 ID Q866J4 PRELIMINARY; PRT; 39 AA.
AC Q866J4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Plasminogen (Fragment).
GN Name=PLG;
OS Aotus trivirgatus (Night monkey) (Douroucoul).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=9505;
RN [1]
RP SEQUENCE FROM N.A.
RA Boffelli D., Lewis K.D., Rubin E.M.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY192763; AAO19630.1; -.
DR HSSP; P00747; IK10.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS50070; KRINGLE_2; 1.
DR KRINGLE.
KW Kringle.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4242 MW; A8DD66BB47090C02 CRC64;

Query Match 53.2%; Score 25; DB 2; Length 39;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYIPA 8
DB 35 GYIPS 39

RESULT 31
Q866J5 ID Q866J5 PRELIMINARY; PRT; 39 AA.
AC Q866J5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Plasminogen (Fragment).
GN Name=PLG;
OS Callithrix sp. DB-2003.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Platyrrhini; Callitrichidae; Callitrix.
OX NCBI_TaxID=217956;
RN [1]
RP SEQUENCE FROM N.A.

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RA Boffelli D., Lewis K.D., Rubin E.M.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY192762; AA019629.1; -.
 DR HSSP; P00747; IKIO.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00051; Kringle; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 KW Kringle.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4300 MW; A8DD66BB44393F02 CRC64;

Query Match 53.2%; Score 25; DB 2; Length 39;
 Best Local Similarity 80.0%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GYIPA 8
 ||||:
 Db 35 GYIPS 39

RESULT 32
 Q866J6 PRELIMINARY; PRT; 39 AA.
 ID Q866J6;
 AC Q866J6;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Plasminogen (Fragment).
 GN Name=PLG;
 OS Alouatta seniculus (Red howler monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Alouattinae;
 OC Alouatta.
 OX NCBI_TaxID=9503;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Boffelli D., Lewis K.D., Rubin E.M.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY192761; AA019628.1; -.
 DR HSSP; P00747; IKIO.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00051; Kringle; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 KW Kringle.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4328 MW; 595466BB44393F10 CRC64;

Query Match 53.2%; Score 25; DB 2; Length 39;
 Best Local Similarity 80.0%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GYIPA 8
 ||||:
 Db 35 GYIPS 39

RESULT 33
 Q866J7 PRELIMINARY; PRT; 39 AA.
 ID Q866J7;
 AC Q866J7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Plasminogen (Fragment).
 GN Name=PLG;
 OS Presbytis entellus (Hanuman langur).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
 OC Presbytis.
 OX NCBI_TaxID=9574;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Boffelli D., Lewis K.D., Rubin E.M.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY192760; AA019627.1; -.
 DR HSSP; P00747; IKIO.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00051; Kringle; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 KW Kringle.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4286 MW; A8DBBDBB44393F02 CRC64;

Query Match 53.2%; Score 25; DB 2; Length 39;
 Best Local Similarity 80.0%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GYIPA 8
 ||||:
 Db 35 GYIPS 39

RESULT 34
 Q866J8 PRELIMINARY; PRT; 39 AA.
 ID Q866J8;
 AC Q866J8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Plasminogen (Fragment).
 GN Name=PLG;
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Boffelli D., Lewis K.D., Rubin E.M.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY192759; AA019626.1; -.
 DR HSSP; P00747; IKIO.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00051; Kringle; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 KW Kringle.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4286 MW; A8DBBDBB44393F02 CRC64;

Query Match 53.2%; Score 25; DB 2; Length 39;
 Best Local Similarity 80.0%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GYIPA 8
 ||||:
 Db 35 GYIPS 39

RESULT 35
 Q866J9 PRELIMINARY; PRT; 39 AA.
 ID Q866J9;
 AC Q866J9;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Plasminogen (Fragment).
 GN Name=PLG;
 OS Gorilla gorilla (gorilla).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN (1)
RP SEQUENCE FROM N.A.
RA Boffelli D., Lewis K.D., Rubin E.M.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY192758; AA019625.1; -.
DR HSSP; P00747; IK10.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 1.
DR PROSITE; PS50070; KRINGLE_2; 1.
KW Kringle.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4286 MW; A8DBDBB44393F02 CRC64;

Query Match 53.2%; Score 25; DB 2; Length 39;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GYIPA 8
Db 35 GYIPS 39

RESULT 36
Q866K0 PRELIMINARY; PRT; 39 AA.
ID Q866K0;
AC Q866K0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Plasminogen (Fragment).
GN Name=PLG;
OS Hylobates lar (Common gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9580;
RN (1)
RP SEQUENCE FROM N.A.
RA Boffelli D., Lewis K.D., Rubin E.M.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY192757; AA019624.1; -.
DR HSSP; P00747; IK10.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 1.
DR PROSITE; PS50070; KRINGLE_2; 1.
KW Kringle.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4286 MW; A8DBDBB44393F02 CRC64;

Query Match 53.2%; Score 25; DB 2; Length 39;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GYIPA 8
Db 35 GYIPS 39

RESULT 37
Q866K1 PRELIMINARY; PRT; 39 AA.
ID Q866K1;
AC Q866K1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Plasminogen (Fragment).
GN Name=PLG;
OS Mandrillus leucophaeus (Drill) (Papio leucophaeus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Mandrillus.
OX NCBI_TaxID=9568;
RN (1)
RP SEQUENCE FROM N.A.
RA Boffelli D., Lewis K.D., Rubin E.M.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY192756; AA019623.1; -.
DR HSSP; P00747; IK10.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS50070; KRINGLE_2; 1.
KW Kringle.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4334 MW; A8DBDBB59E8F202 CRC64;

Query Match 53.2%; Score 25; DB 2; Length 39;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GYIPA 8
Db 35 GYIPS 39

RESULT 38
Q866K2 PRELIMINARY; PRT; 39 AA.
ID Q866K2;
AC Q866K2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Plasminogen (Fragment).
GN Name=PLG;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN (1)
RP SEQUENCE FROM N.A.
RA Boffelli D., Lewis K.D., Rubin E.M.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY192755; AA019622.1; -.
DR HSSP; P00747; IK10.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 1.
DR PROSITE; PS50070; KRINGLE_2; 1.
KW Kringle.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4286 MW; A8DBDBB44393F02 CRC64;

Query Match 53.2%; Score 25; DB 2; Length 39;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GYIPA 8
Db 35 GYIPS 39

RESULT 39
Q866K3 PRELIMINARY; PRT; 39 AA.
ID Q866K3;
AC Q866K3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Plasminogen (Fragment).
GN Name=PLG;
OS Allenopithecus nigroviridis (Allen's swamp monkey).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Cercopithecidae;
 OC NCBI_TaxID=54135;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Boffelli D., Lewis K.D., Rubin E.M.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY192754; A0019621.1; -.
 DR HSSP; P00747; 1K10.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00051; Kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PSS0070; KRINGLE_2; 1.
 KW Kringle.
 FT NON TER 1 1
 FT NON TER 39 39
 SQ SEQUENCE 39 AA; 4286 MW; A8DBBBB44393F02 CRC64;
 Query Match 53.2%; Score 25; DB 2; Length 39;
 Best Local Similarity 80.0%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 GYIPA 8
 Db 35 GYIPS 39
 RESULT 40
 Q91K22
 ID Q91K22 PRELIMINARY; PRT; 40 AA.
 AC Q91K22
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Polyprotein (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OC NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2132446; PubMed=11431747; DOI=10.1053/jhep.2001.25512;
 RA Gimenez-Barcons M., Franco S., Suarez X., Fornis X., Ampurdanes S.,
 RA Puig-Basagot F., Sanchez-Fuero A., Barrera J.M., Llovet J.M.,
 RA Bruix J., Sanchez-Tapias J.M., Rodes J., Saiz J.C.;
 RT "High amino acid variability within the NS5A of hepatitis C virus
 (HCV) is associated with hepatocellular carcinoma in patients with
 HCV-1b-related cirrhosis.";
 RT Hepatology 34:158-167(2001).
 RL EMBL; AF379250; AAK63467.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR Pfam; PF01560; HCV NS1; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 FT NON TER 1 1
 FT NON TER 40 40
 SQ SEQUENCE 40 AA; 4162 MW; F8ECD3FE433B812E CRC64;
 Query Match 53.2%; Score 25; DB 2; Length 40;
 Best Local Similarity 57.1%; Pred. No. 2.8e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 LMGVIPA 8
 Db 4 LMGVIPA 10

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 13:24:58 ; Search time 39 Seconds
(without alignments)
22.204 Million cell updates/sec

Title: US-10-770-117-1

Perfect score: 47

Sequence: 1 DLGVIIPAV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 79:*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	57.4	27	4 JE0015	probable 2.8K prot
2	27	57.4	27	4 JS0104	probable 2.8K prot
3	26	55.3	24	2 T42390	phosphoprotein pho
4	26	55.3	40	2 A82529	hypothetical prote
5	26	55.3	44	2 T42124	probable regulator
6	25	53.2	21	2 S35676	protein kinase - r
7	25	53.2	24	2 A61505	pollen allergen ph
8	25	53.2	27	2 S05219	photosystem I chai
9	25	53.2	31	2 AF0736	hypothetical prote
10	24	51.1	16	2 B36300	T-cell receptor de
11	24	51.1	33	2 D36204	GTP-binding regula
12	24	51.1	36	2 S22222	probable lipid tra
13	24	51.1	49	2 T44523	hypothetical prote
14	23	48.9	16	2 S38292	30K allergen - rye
15	23	48.9	19	2 S71871	glutathione transf
16	23	48.9	20	2 S38288	50K allergen - per
17	23	48.9	20	2 S38294	32K allergen - com
18	23	48.9	20	2 S38291	30K allergen - vel
19	23	48.9	33	2 H82216	hypothetical prote
20	23	48.9	34	2 A55758	myosin - human (fr
21	23	48.9	35	2 A61077	glue protein - rib
22	23	48.9	38	2 PS0339	immunoglobulin-bin
23	23	48.9	38	2 E81889	hypothetical prote
24	23	48.9	45	2 G95916	hypothetical exope
25	23	48.9	46	2 I40735	ltuA protein - chl
26	22	46.8	46	2 D81678	conserved hypothet
27	22	46.8	17	2 PH1312	Ig heavy chain DJ
28	22	46.8	20	2 A05332	serum amyloid P-co
29	22	46.8	20	2 S06149	photosystem I chai

30	22	46.8	21	2 S21772	lipoxigenase (EC 1
31	22	46.8	26	2 E27011	MHC class II-assoc
32	22	46.8	30	2 C43591	51K outer membrane
33	22	46.8	33	2 E84341	hypothetical prote
34	22	46.8	36	2 I46593	myosin - pig (frag
35	22	46.8	37	2 S03941	hydrogen dehydroge
36	22	46.8	42	2 A30010	cytochrome-c oxida
37	22	46.8	43	2 PS0359	hypothetical prote
38	22	46.8	44	2 C35156	dihydrolipoamide d
39	22	46.8	45	2 B35156	dihydrolipoamide d
40	22	46.8	48	2 S16924	cytochrome cc3 - D
41	22	46.8	48	2 S11639	hypothetical prote
42	22	46.8	49	2 I38067	nitric-oxide synth
43	21	44.7	24	2 S34405	adenylate kinase (
44	21	44.7	25	2 S03275	photosystem II 22K
45	21	44.7	29	2 G90719	hypothetical prote
46	21	44.7	29	2 T48910	KDPF protein [vali
47	21	44.7	29	2 T36654	probable small mem
48	21	44.7	34	2 F86055	hypothetical prote
49	21	44.7	35	2 S42673	adhesive protein -
50	21	44.7	37	2 A10933	coagulation factor
51	21	44.7	37	2 F82102	hypothetical prote
52	21	44.7	38	2 S32314	sinapine synthase
53	21	44.7	39	2 F97313	hypothetical prote
54	21	44.7	40	2 C69400	hypothetical prote
55	21	44.7	41	2 PX0046	GTP-binding protei
56	21	44.7	42	2 G90273	hypothetical prote
57	21	44.7	44	2 E82479	hypothetical prote
58	21	44.7	45	2 H70240	hypothetical prote
59	21	44.7	45	2 H97508	hypothetical prote
60	21	44.7	47	2 T37087	probable IS elemen
61	21	44.7	47	2 AF1165	Hypothetical CDS [
62	21	44.7	48	2 A38882	GTP-binding protei
63	21	44.7	48	2 S26102	outer membrane pro
64	21	44.7	48	2 A35156	dihydrolipoamide d
65	21	44.7	49	2 T06923	high light-inducib
66	21	44.7	49	2 T40034	probable mitochond
67	21	44.7	49	2 C90080	hypothetical prote
68	20.5	43.6	40	2 A43853	fructose-bisphosph
69	20	42.6	9	2 S13636	coat protein beta
70	20	42.6	15	2 A36279	chemoattractant pr
71	20	42.6	18	2 A35704	cytochrome P450 ol
72	20	42.6	19	2 A41668	integrin alpha-7 c
73	20	42.6	20	2 A61525	alpha-lactalbumin
74	20	42.6	21	2 I50535	calmodulin - elect
75	20	42.6	22	2 I50533	calmodulin - elect
76	20	42.6	22	2 S55308	glutathione transf
77	20	42.6	23	2 S23518	stromelysin (EC 3.
78	20	42.6	23	2 FC4030	rRNA endonuclease
79	20	42.6	25	2 A61457	alpha-glucosidase
80	20	42.6	30	2 G81031	hypothetical prote
81	20	42.6	30	2 S57227	proboscipedia prot
82	20	42.6	31	2 B98020	N-acetylneuraminat
83	20	42.6	31	2 B98061	N-acetylneuraminat
84	20	42.6	33	2 PS0433	dystrophin - rabbi
85	20	42.6	34	2 S34265	hypothetical prote
86	20	42.6	36	1 F1FNIT	histidyl-tRNA synt
87	20	42.6	36	2 T38913	photosystem I prot
88	20	42.6	36	2 S73308	photosystem I chai
89	20	42.6	36	2 S01531	photosystem I prot
90	20	42.6	37	1 S26087	plastoquinol-plast
91	20	42.6	37	2 S73239	conserved hypothet
92	20	42.6	37	2 D69283	Ivi protein III -
93	20	42.6	38	2 S70800	hypothetical prote
94	20	42.6	38	2 B71349	rex protein - simi
95	20	42.6	39	2 S44288	CAB/ELIP/HLP-rela
96	20	42.6	40	2 A41862	hypothetical prote
97	20	42.6	40	2 E64039	hypothetical prote
98	20	42.6	41	2 T45906	hypothetical prote
99	20	42.6	42	2 T07474	hypothetical prote
100	20	42.6	43	2 E54252	omega-agatoxin III

ALIGNMENTS

RESULT 1

JE0015
 C:Species: cucurbit mosaic virus (strain D)
 C:Date: 31-Dec-1991 #sequence_revision 28-May-1998 #text_change 09-Jul-2004
 C:Accession: JE0015; PS0286
 R:Richards, K.E.; Jonard, G.; Jacquemond, M.; Lot, H.
 Virolgy 89, 395-408, 1978
 A:Title: Nucleotide sequence of cucumber mosaic virus-associated RNA 5.
 A:Reference number: JE0015
 A:Accession: JE0015
 A:Status: translation not shown; conceptual translation of pseudogene
 A:Molecule type: genomic RNA
 A:Residues: 1-27 <RIC>
 A:Cross-references: UNIPROT:Q89492
 R:Kaper, J.M.; Tournant, M.E.; Steen, M.T.
 Virology 163, 284-292, 1988
 A:Title: Cucurbit mosaic virus-associated RNA 5. XI. Comparison of 14 CARNA 5 variants
 A:Reference number: JE0018; MUID:88179532; PMID:3354198
 A:Accession: PS0286
 A:Status: translation not shown; conceptual translation of pseudogene
 A:Molecule type: genomic RNA
 A:Residues: 1-27 <KAP>
 A:Cross-references: GB:M20350; NID:G331658; PIDN:AAA46385.1; PID:G331659
 A:Note: this sequence is found in strain D and isolates Sq10, Ch20, X2nt3, X7, X12 and X
 C:Genetics:
 A:Map position: segment 5
 C:Keywords: pseudogene

Query Match 57.4%; Score 27; DB 4; Length 27;
 Best Local Similarity 66.7%; Pred. No. 94;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MGYP1A 8

Db 19 VGYP1A 24

RESULT 2

JS0104
 Probable 2.8K protein pseudogene - cucumber mosaic virus (strain Y)
 C:Species: cucumber mosaic virus, CMV
 A:Note: host Nicotiana tabacum cv. Xanthi nc (tobacco)
 C:Date: 31-Mar-1992 #sequence_revision 28-May-1998 #text_change 09-Jul-2004
 C:Accession: JS0104
 R:Hidaka, S.; Ishikawa, K.; Takanami, Y.; Kubo, S.; Miura, K.
 FEBS Lett. 174, 38-42, 1984
 A:Title: Complete nucleotide sequence of RNA 5 from cucumber mosaic virus (strain Y).
 A:Reference number: JA0077
 A:Accession: JS0104
 A:Status: translation not shown; conceptual translation of pseudogene
 A:Molecule type: genomic RNA
 A:Residues: 1-27 <HID>
 A:Cross-references: UNIPROT:Q89492
 C:Comment: CMV is an icosahedral virus containing a tripartite, positive-stranded RNA ge
 nent referred to as satellite RNA.
 C:Genetics:
 A:Map position: segment 5
 C:Keywords: pseudogene

Query Match 57.4%; Score 27; DB 4; Length 27;
 Best Local Similarity 66.7%; Pred. No. 94;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MGYP1A 8

Db 19 VGYP1A 24

RESULT 3

T42124
 Probable regulatory protein - Escherichia coli plasmid p0157
 C:Species: Escherichia coli

T42390

Phosphoprotein phosphatase (EC 3.1.3.16) - Caenorhabditis elegans (fragment)
 C:Species: Caenorhabditis elegans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T42390
 R:Zeke, T.; Gergely, P.; Dombradi, V.
 submitted to the EMBL Data Library, July 1996
 A:Description: The catalytic subunits of Ser/Thr protein phosphatases from Caenorhabditis
 A:Reference number: Z22131
 A:Accession: T42390
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-24 <ZEK>
 A:Cross-references: UNIPROT:Q94370; EMBL:Z77730; PIDN:CAB01289.1
 C:Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phosph
 C:Keywords: phosphoric monoester hydrolase

Query Match 55.3%; Score 26; DB 2; Length 24;
 Best Local Similarity 55.6%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9

Db 10 DAVGYPPKV 18

RESULT 4

AB2529
 hypothetical protein XF2678 [imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: AB2529
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: AB2515; MUID:20365717; PMID:10910347
 A:Note: for a complete list of authors see reference number AB2529 below
 A:Accession: AB2529
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-40 <SIM>
 A:Cross-references: UNIPROT:Q9PA42; GB:AE004073; GB:AE003849; NID:g9107904; PIDN:AAF8547;
 A:Experimental source: strain 9a5c
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigre
 Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A:Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: AB2528
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF2678

Query Match 55.3%; Score 26; DB 2; Length 40;
 Best Local Similarity 50.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LMGYP1AV 9

Db 3 LMGYVESV 10

RESULT 5

T42124
 Probable regulatory protein - Escherichia coli plasmid p0157
 C:Species: Escherichia coli

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: T42124
 R;Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
 Nucleic Acids Res. 26, 4196-4204, 1998
 A;Title: The complete DNA sequence and analysis of the large virulence plasmid of *Escherichia coli* O157:H7
 A;Reference number: 222068; MUID:98391744; PMID:9722640
 A;Accession: T42124
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-44

 A;Cross-references: UNIPROT:Q9ZGU6; EMBL:AF074613; PIDN:AAC70092.1
 A;Experimental source: strain BDL933; serotype O157:H7
 C;Genetics:
 A;Genome: plasmid pO157
 A;Note: L7024
 C;Superfamily: type 1 fimbriae regulatory protein fimE
 C;Keywords: transcription regulation

Query Match 55.3%; Score 26; DB 2; Length 44;
 Best Local Similarity 62.5%; Pred. No. 2.4e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LMGYIPAV 9
 |||||
 Db 12 LMGYLHGV 19

RESULT 6
 S35676
 protein kinase - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S35676
 R;Brunati, A.M.; James, P.; Donella-Deana, A.; Matoskova, B.; Robbins, K.C.; Pinna, L.A.
 Eur. J. Biochem. 216, 323-327, 1993
 A;Title: Isolation and identification of two proto-oncogene products related to c-fgr an
 A;Reference number: S35675; MUID:93373942; PMID:8365414
 A;Accession: S35676
 A;Molecule type: protein
 A;Residues: 1-21

 A;Cross-references: UNIPROT:Q7M035

Query Match 53.2%; Score 25; DB 2; Length 21;
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GYIPA 8
 |||||
 Db 15 GYIPS 19

RESULT 7
 A61505
 pollen allergen phi p v - common timothy (fragment)
 C;Species: Phleum pratense (common timothy)
 C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
 C;Accession: A61505
 R;Matthiesen, F.; Lowenstein, H.
 Clin. Exp. Allergy 21, 297-307, 1991
 A;Title: Group V allergens in grass pollens. I. Purification and characterization of the
 A;Reference number: A61505; MUID:91322736; PMID:1863892
 A;Accession: A61505
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-24 <MAT>
 A;Cross-references: UNIPROT:Q7M1L8
 A;Note: 2-Ala, 5-Gly, and 15-Glu were also found
 C;Superfamily: grass pollen allergen IX
 C;Keywords: hydroxyproline; pollen
 P;6,9,12,18,21,24/Modified site: hydroxyproline (Pro) #status experimental

Query Match 53.2%; Score 25; DB 2; Length 24;
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 MGYIPA 8
 :|||
 Db 2 LGIAPA 7

RESULT 8
 S05219
 photosystem I chain III - *Synechococcus* sp. (fragment)
 N;Alternate names: photosystem I L4K protein; photosystem I plastocyanin-binding chain
 C;Species: *Synechococcus* sp.
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 30-Apr-1999
 C;Accession: S05219
 R;Koike, H.; Ikeuchi, M.; Hiyama, T.; Inoue, Y.
 FEBS Lett. 253, 257-263, 1989
 A;Title: Identification of photosystem I components from the cyanobacterium, *Synechococcus*
 A;Reference number: S05218; MUID:89338747; PMID:2503399
 A;Accession: S05219
 A;Molecule type: protein
 A;Residues: 1-27 <KOI>
 A;Note: the authors identified this protein as photosystem I chain IV
 R;Koike, H.; Ikeuchi, M.; Hiyama, T.; Inoue, Y.
 FEBS Lett. 258, 180B, 1989
 A;Reference number: S06842
 A;Contents: annotation; erratum
 A;Note: this is a revision to the identification of the sequence in reference S05218
 C;Genetics:
 A;Gene: psaf
 C;Superfamily: photosystem I chain III
 C;Keywords: photosynthesis; photosystem I; thylakoid

Query Match 53.2%; Score 25; DB 2; Length 27;
 Best Local Similarity 50.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DLMGYIPA 8
 :|||
 Db 1 DVAGLVP 8

RESULT 9
 AF0736
 hypothetical protein STY2049 [imported] - *Salmonella enterica* subsp. *enterica* serovar Ty
 C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
 A;Note: this species has also been called *Salmonella typhi*
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AF0736
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* sero
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AF0736
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-31 <PAR>
 A;Cross-references: GB:AL513382; PIDN:CAD05592.1; PID:gl503089; GSPDB:GN00176
 C;Genetics:
 A;Gene: STY2049

Query Match 53.2%; Score 25; DB 2; Length 31;
 Best Local Similarity 66.7%; Pred. No. 2.7e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LMGYIP 7
 :|||
 Db 7 IRGYIP 12

RESULT 10

B36300
T-cell receptor delta chain V-J region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 30-May-1997
C:Accession: B36300
R:Matlis, L.A.; Fry, A.M.; Cron, R.Q.; Cotterman, M.M.; Dick, R.F.; Bluestone, J.A.
Science 245, 746-749, 1999
A:Title: Structure and specificity of a class II MHC alloreactive gammadelta T cell receptor
A:Reference number: A36300; MUID:89368895; PMID:2528206
C:Accession: B36300
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-16 <MAT>
C:Keywords: T-cell receptor

Query Match 51.1%; Score 24; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GYIP 7
Db 3 GYIP 6

RESULT 11
D36204
GTP-binding regulatory protein gamma-2 chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 19-Jul-1996
C:Accession: D36204
R:Gautam, N.; Northup, J.; Tamir, H.; Simon, M.I.
Proc. Natl. Acad. Sci. U.S.A. 87, 7973-7977, 1990
A:Title: G protein diversity is increased by associations with a variety of gamma subunits
A:Reference number: A36204; MUID:91045919; PMID:2122451
C:Accession: D36204
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-33 <GAU>
C:Superfamily: GTP-binding regulatory protein gamma chain

Query Match 51.1%; Score 24; DB 2; Length 33;
Best Local Similarity 62.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DLMGYIPA 8
Db 15 DLMAYCEA 22

RESULT 12
S22222
probable lipid transfer protein - Italian stone pine (fragment)
C:Species: Pinus pinea (Italian stone pine)
C:Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 09-Jul-2004
C:Accession: S22222
R:Polya, G.M.; Chandra, S.; Chung, R.; Neumann, G.M.; Hoej, P.B.
Biochim. Biophys. Acta 1120, 273-280, 1992
A:Title: Purification and characterization of wheat and pine small basic protein subunits
A:Reference number: S21748; MUID:92247807; PMID:1576154
C:Accession: S22222
A:Molecule type: protein
A:Residues: 1-36 <POL>
A:Cross-references: UNIPROT:P25912
A:Experimental source: seed
C:Function:
A:Description: involved in the phospholipid transfer
C:Superfamily: phospholipid transfer protein
C:Keywords: lipid transport; phospholipid

Query Match 51.1%; Score 24; DB 2; Length 36;
Best Local Similarity 50.0%; Pred. No. 5e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MGYIPA 8
Db 15 VGYLPS 20

RESULT 13
T44523
hypothetical protein 4S [imported] - Shigella sonnei (fragment)
C:Species: Shigella sonnei
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T44523
R:Chida, T.; Okamura, N.; Yoshida, Y.; Ohtani, K.; Arakawa, E.; Watanabe, H.
submitted to the EMBL Data Library, May 1999
A:Description: Complete DNA sequence of the O-antigen (rfb) gene cluster in Plesiomonas shigelloides
A:Reference number: Z22787
A:Accession: T44523
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-49 <CHI>
A:Cross-references: UNIPROT:Q9S0U2; EMBL:AB028135; FIDN:BAA85074.1
A:Experimental source: isolate HW383

Query Match 51.1%; Score 24; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GYIP 7
Db 36 GYIP 39

RESULT 14
S38292
30K allergen - rye (fragment)
C:Species: Secale cereale (rye)
C:Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C:Accession: S38292
R:Petersen, A.; Schramm, G.; Becker, W.M.; Schlaak, M.
Biol. Chem. Hoppe-Seyler 374, 855-861, 1993
A:Title: Comparison of four grass pollen species concerning their allergens of grass group 1
A:Reference number: S38288; MUID:94092339; PMID:7505588
C:Accession: S38292
A:Molecule type: protein
A:Residues: 1-16 <PET>
A:Cross-references: UNIPROT:Q7M263

Query Match 48.9%; Score 23; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GYIPA 8
Db 4 GYAPA 8

RESULT 15
S71871
glutathione transferase (EC 2.5.1.18) class mu 10 - pig (fragments)
N:Alternate names: glutathione S-transferase class mu 10
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C:Accession: S71871
R:Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.
Biochem. J. 317, 879-884, 1996
A:Title: Characterization of pig liver glutathione S-transferases using HPLC-electrophoresis
A:Reference number: S71864; MUID:96332484; PMID:8760377
C:Accession: S71871
A:Molecule type: protein
A:Residues: 1-19 <ROU>
C:Comment: At least five species-independent classes of cytosolic glutathione transferases
s mitochondrial form are known.
C:Complex: dimer
C:Function:

A;Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a
 A;Pathway: detoxification; xenobiotics metabolism
 A;Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism
 es of damage
 C;Superfamily: glutathione transferase
 C;Keywords: dimer; transferase

Query Match 48.9%; Score 23; DB 2; Length 19;
 Best Local Similarity 60.0%; Pred. No. 4.1e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLMGY 5
 Db 2 DILGY 6

RESULT 16

S38288
 50K allergen - perennial ryegrass (fragment)
 C;Species: Lolium perenne (perennial ryegrass)
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C;Accession: S38288
 R;Petersen, A.; Schramm, G.; Becker, W.M.; Schlaak, M.
 Biol. Chem. Hoppe-Seyler 374, 855-861, 1993
 A;Title: Comparison of four grass pollen species concerning their allergens of grass gro
 A;Reference number: S38288; MUID:94092339; PMID:7505588
 A;Accession: S38288
 A;Molecule type: protein
 A;Residues: 1-20 <PET>
 A;Cross-references: UNIPROT:Q7M264

Query Match 48.9%; Score 23; DB 2; Length 20;
 Best Local Similarity 80.0%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GYIPA 8
 Db 4 GYAPA 8

RESULT 17

S38294
 32K allergen - common timothy (fragment)
 C;Species: Phleum pratense (common timothy)
 C;Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
 C;Accession: S38294
 R;Petersen, A.; Schramm, G.; Becker, W.M.; Schlaak, M.
 Biol. Chem. Hoppe-Seyler 374, 855-861, 1993
 A;Title: Comparison of four grass pollen species concerning their allergens of grass gro
 A;Reference number: S38288; MUID:94092339; PMID:7505588
 A;Accession: S38294
 A;Molecule type: protein
 A;Residues: 1-20 <PET>
 A;Cross-references: UNIPROT:Q9S8X9

Query Match 48.9%; Score 23; DB 2; Length 20;
 Best Local Similarity 80.0%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GYIPA 8
 Db 4 GYAPA 8

RESULT 18

S38291
 30K allergen - velvet grass (fragment)
 C;Species: Holcus lanatus (velvet grass)
 C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
 C;Accession: S38291
 R;Petersen, A.; Schramm, G.; Becker, W.M.; Schlaak, M.
 Biol. Chem. Hoppe-Seyler 374, 855-861, 1993
 A;Title: Comparison of four grass pollen species concerning their allergens of grass gro

A;Reference number: S38288; MUID:94092339; PMID:7505588
 A;Accession: S38291
 A;Molecule type: protein
 A;Residues: 1-20 <PET>
 A;Cross-references: UNIPROT:Q7M262

Query Match 48.9%; Score 23; DB 2; Length 20;
 Best Local Similarity 80.0%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GYIPA 8
 Db 4 GYTPA 8

RESULT 19

H82216
 hypothetical protein VCI292 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C;Species: Vibrio cholerae
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: H82216
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
 I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Accession: H82216
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-33 <HEI>
 A;Cross-references: UNIPROT:Q9KSG4; GB:AE004209; GB:AE003852; NID:G9655779; PIDN:AAF9445
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VCI292
 A;Map position: 1

Query Match 48.9%; Score 23; DB 2; Length 33;
 Best Local Similarity 80.0%; Pred. No. 7.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GYIPA 8
 Db 9 GHIPA 13

RESULT 20

A55758
 myosin - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
 C;Accession: A55758
 R;Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
 Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
 A;Title: Identification and overlapping expression of multiple unconventional myosin gen
 A;Reference number: A55758; MUID:94294418; PMID:8022818
 A;Accession: A55758
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-34 <RES>
 A;Cross-references: UNIPROT:Q13871; GB:L29137; NID:G457231; PIDN:AAA20900.1; PID:G531130
 C;Superfamily: brush border myosin heavy chain I; myosin motor domain homology

Query Match 48.9%; Score 23; DB 2; Length 34;
 Best Local Similarity 50.0%; Pred. No. 7.5e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LMGYIPAV 9
 Db 6 VMSYVAAV 13

RESULT 21

A61077
 Glue protein - ribbed mussel (fragments)
 C;Species: Geukensia demissa (ribbed mussel)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C;Accession: A61077
 R;Waite, J.H.; Hansen, D.C.; Little, K.T.
 J. Comp. Physiol. B 159, 517-525, 1989
 A;Title: The glue protein of ribbed mussels (Geukensia demissa): a natural adhesive with
 A;Reference number: A61077; MUID:90110595; PMID:2481690
 A;Accession: A61077
 A;Molecule type: protein
 A;Residues: 1-35 <WAI>
 A;Cross-references: UNIPROT:Q7M3X7
 C;Superfamily: glutenin
 C;Keywords: hydroxyllysine; hydroxyproline; tandem repeat
 F;3,7,12,21/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental
 F;14/Modified site: 4-hydroxyproline (Pro) #status experimental
 F;16,30,34/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) (partial) #status experimental

Query Match 48.9%; Score 23; DB 2; Length 35;
 Best Local Similarity 75.0%; Pred. No. 7.7e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYIP 7
 Db 11 GYVP 14

RESULT 22
 PS0339
 immunoglobulin-binding 30K protein - Pseudomonas maltophilia (fragments)
 C;Species: Pseudomonas maltophilia
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C;Accession: PS0339
 R;Grover, S.; Odell, W.D.
 Biochem. Biophys. Res. Commun. 182, 1075-1081, 1992
 A;Title: Partial characterization of the 30 KD Ig-binding protein from Pseudomonas malt
 A;Reference number: PS0339; MUID:92171911; PMID:1540156
 A;Accession: PS0339
 A;Molecule type: protein
 A;Residues: 1-38 <GRO>
 A;Cross-references: UNIPROT:Q7M0Q2
 C;Comment: This cell wall protein binds the Fc region of immunoglobulin G.

Query Match 48.9%; Score 23; DB 2; Length 38;
 Best Local Similarity 75.0%; Pred. No. 8.4e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYIP 7
 Db 12 GYVP 15

RESULT 23
 E81889
 hypothetical protein NMA1214 [imported] - Neisseria meningitidis (strain Z2491 serogroup
 C;Species: Neisseria meningitidis
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C;Accession: E81889
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 ; Holroyd, S.; Jogle, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A;Reference number: A81775; MUID:20222556; PMID:10761919
 A;Accession: E81889
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-38 <PAR>
 A;Cross-references: UNIPROT:Q9JUP1; GB:AL162755; GB:AL157959; NID:G7379742; PIDN:CAB8447
 A;Experimental source: serogroup A, strain Z2491
 C;Genetics:
 A;Gene: NMA1212; NMA1214

Query Match 48.9%; Score 23; DB 2; Length 38;
 Best Local Similarity 55.8%; Pred. No. 8.4e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLGGYIPAV 9
 Db 24 EMIIYYPVAV 32

RESULT 24
 G95916
 hypothetical exopeptide protein [imported] - Sinorhizobium meliloti (strain 1021) magapla
 C;Species: Sinorhizobium meliloti
 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C;Accession: G95916
 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A;Title: The complete sequence of the 1.683-kb pSymb
 A;Reference number: A95842; MUID:21396508; PMID:11481431
 A;Accession: G95916
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-45 <KUR>
 A;Cross-references: UNIPROT:Q92VU9; GB:AL591985; PIDN:CAC48999.1; PID:g15140484; GSPDB:G
 A;Experimental source: strain 1021, megaplasmid pSymb
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler,
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A;Reference number: A96039; MUID:21368234; PMID:11474104
 A;Contents: annotation
 C;Genetics:
 A;Gene: Smb21026
 A;Genome: plasmid

Query Match 48.9%; Score 23; DB 2; Length 45;
 Best Local Similarity 33.3%; Pred. No. 1e+03;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 LMGYIP 7
 Db 22 ILGFVP 27

RESULT 25
 I40735
 ltua protein - Chlamydia trachomatis (serotype D, strain UW3/Cx)
 C;Species: Chlamydia trachomatis
 C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
 C;Accession: I40735; E71521
 R;Fahr, M.J.; Douglas, A.L.; Xia, W.; Hatch, T.P.
 J. Bacteriol. 177, 4252-4260, 1995
 A;Title: Characterization of late gene promoters of Chlamydia trachomatis.
 A;Reference number: I40734; MUID:95362647; PMID:7543468
 A;Accession: I40735
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-46 <RES>
 A;Cross-references: UNIPROT:Q46403; GB:IL40822; NID:9886216; PIDN:AAA75629.1; PID:9886218
 R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
 Science 282, 754-759, 1998
 A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tract
 A;Reference number: A71570; MUID:99000809; PMID:9784136
 A;Accession: E71521
 A;Molecule type: DNA
 A;Residues: 1-46 <ARN>
 A;Cross-references: GB:AE001311; GB:AE001273; NID:G3328799; PIDN:AA67973.1; PID:G3328802
 A;Experimental source: serotype D, strain UW-3/Cx
 C;Genetics:
 A;Gene: ltua

Query Match 48.9%; Score 23; DB 2; Length 46;
Best Local Similarity 50.0%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DLMGYIPA 8
| : | : |
Db 13 DVHGYLAA 20

RESULT 26
D81678
conserved hypothetical protein TC0656 [imported] - Chlamydia muridarum (strain Nigg)
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: D81678
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: D81678
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-46 <TET>
A:Cross-references: UNIPROT:Q9PK17; GB:AE002334; GB:AE002160; NID:g7190690; PIDN:AAF3948
A:Experimental source: strain Nigg (MoPn)
C:Genetics:
A:Gene: TC0656

Query Match 48.9%; Score 23; DB 2; Length 46;
Best Local Similarity 50.0%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DLMGYIPA 8
| : | : |
Db 13 DVHGYLAA 20

RESULT 27
PH1312
Ig heavy chain DJ region (clone C68-105) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1312
R:Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma.
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1312
A:Molecule type: DNA
A:Residues: 1-17 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match 46.8%; Score 22; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YIPA 8
| : | : |
Db 7 YIPA 10

RESULT 28
A05332
serum amyloid P-component - plaice (fragment)
N:Alternate names: SAP
C:Species: Pleuronectes platessa (plaice)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C:Accession: A05332
R:Pepys, M.B.; de Beer, F.C.; Milstein, C.P.; March, J.F.; Feinstein, A.; Butress, N.; C
Biochim. Biophys. Acta 704, 123-133, 1982
A:Reference number: A90642; MUID:82232106; PMID:7093286

A:Contents: tentative sequence
A:Accession: A05332
A:Molecule type: protein
A:Residues: 1-20 <PEP>
A:Cross-references: UNIPROT:P20677
C:Superfamily: C-reactive protein
C:Keywords: amyloid; glycoprotein; pentraxin; plasma

Query Match 46.8%; Score 22; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 6.9e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYI 6
| : | : |
Db 4 DLMGKV 9

RESULT 29
S06149
photosystem I chain III - barley (fragment)
C:Species: Hordeum vulgare (barley)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C:Accession: S06149
R:Anandan, S.; Vainstein, A.; Thornber, J.P.
FEBS Lett. 256, 150-154, 1989
A:Title: Correlation of some published amino acid sequences for photosystem I polypeptide
A:Reference number: S06149; MUID:90033290; PMID:2680596
A:Accession: S06149
A:Molecule type: protein
A:Residues: 1-20 <ANA>
A:Note: the authors identified this protein as light-harvesting complex I 17K protein
C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 46.8%; Score 22; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 6.9e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DLMGYIPA 8
| : | : |
Db 1 DIAGLTPA 8

RESULT 30
S21772
lipoxigenase (EC 1.13.11.12) 1 - barley (fragment)
C:Species: Hordeum vulgare (barley)
C:Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C:Accession: S21772
R:Doderer, A.; Kokkelink, I.; van der Veen, S.; Valk, B.E.; Schram, A.W.; Douma, A.C.
Biochim. Biophys. Acta 1120, 97-104, 1992
A:Title: Purification and characterization of two lipoxigenase isoenzymes from germinating
A:Reference number: S21772; MUID:92207997; PMID:1554746
A:Accession: S21772
A:Molecule type: protein
A:Residues: 1-21 <DOD>
A:Experimental source: var. Triumph, seed
C:Function:
A:Description: catalyzes the peroxidation of polyunsaturated fatty acids to their corres
C:Superfamily: lipoxigenase
C:Keywords: monomer; oxidoreductase; seed

Query Match 46.8%; Score 22; DB 2; Length 21;
Best Local Similarity 66.7%; Pred. No. 7.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GYIPAV 9
| : | : |
Db 5 GILPAV 10

RESULT 31
E27011
MHC class II-associated invariant chain - human

C;Species: Homo sapiens (man)
C;Date: 21-Nov-1987 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: S40464; E27011
R;Ogrinc, T.; Dolenc, I.; Ritonja, A.; Turk, V.
FEBS Lett. 336, 555-559, 1993
A;Title: Purification of the complex of cathepsin L and the MHC class II-associated invariant chain from human neutrophils
A;Reference number: S40464; MUID:94109606; PMID:8282126
A;Accession: S40464
A;Molecule type: protein
A;Residues: 1-26 <OGR>
A;Cross-references: UNIPROT:O78208
R;Machleidt, W.; Ritonja, A.; Popovic, T.; Kotnik, M.; Brzin, J.; Turk, V.; Machleidt, H.
in Cysteine Proteinases and Their Inhibitors, Turk, V., ed., pp 3-18, Walter de Gruyter, Berlin, 1994
A;Title: Human cathepsins B, H and L: Characterization by amino acid sequences and some properties
A;Reference number: A27011
A;Accession: E27011
A;Molecule type: protein
A;Residues: 'X', '2', '3', 'G', '5-6', 'G', '8-21' <MAC>
C;Superfamily: class II histocompatibility antigen-associated gamma chain; thyroglobulin

Query Match 46.8%; Score 22; DB 2; Length 26;
Best Local Similarity 57.1%; Pred. No. 9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 MGYIPAV 9
: : |||||
Db 8 VSHIPAV 14

RESULT 32
C43591
51K outer membrane protein - Wolinella recta (ATCC 33238) (fragment)
C;Species: Wolinella recta
C;Date: 12-Jan-1993 #sequence_revision 12-Jan-1993 #text_change 17-Nov-2000
C;Accession: C43591
R;Kennell, W.L.; Holt, S.C.
Infect. Immun. 59, 3740-3749, 1991
A;Title: Extraction, purification, and characterization of major outer membrane proteins of Wolinella recta
A;Reference number: A43591; MUID:91372989; PMID:1894372
A;Accession: C43591
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-30 <KEN>
C;Superfamily: Campylobacter jejuni major outer membrane porin
C;Keywords: membrane protein

Query Match 46.8%; Score 22; DB 2; Length 30;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DLMGY 5
: : |||
Db 11 DLSGY 15

RESULT 33
E84341
hypothetical protein Vng1904h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: E84341
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabczyk, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lindberg, M.P.
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: E84341
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-33 <STO>
A;Cross-references: UNIPROT:Q9HMX3; GB:AE004437; NID:g10581346; PIDN:AAG20097.1; GSPDB:G

C;Genetics:
A;Gene: VNG1904H

Query Match 46.8%; Score 22; DB 2; Length 33;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DLMGYIPAV 9
: : |||
Db 18 ELLGDLFPV 26

RESULT 34
I46593
myosin - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46593
R;Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
A;Title: Identification and overlapping expression of multiple unconventional myosin genes from the pig
A;Reference number: A55758; MUID:94294418; PMID:8022818
A;Accession: I46593
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-36 <BEM>
A;Cross-references: UNIPROT:Q29059; GB:L29128; NID:g457338; PIDN:AAA20913.1; PID:G531144
C;Superfamily: brush border myosin heavy chain I; myosin motor domain homology

Query Match 46.8%; Score 22; DB 2; Length 36;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LMGYIPAV 9
: : |||
Db 6 IMQYIAAI 13

RESULT 35
S03941
hydrogen dehydrogenase (EC 1.12.1.2) alpha chain, cytosolic - Rhodococcus sp. (fragment)
N;Alternate names: NAD-linked hydrogenase alpha chain
C;Species: Rhodococcus sp.
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Apr-2000
C;Accession: S03941
R;Zaborosch, C.; Schneider, K.; Schlegel, H.G.; Kratzin, H.
Eur. J. Biochem. 181, 175-180, 1989
A;Title: Comparison of the NH(2)-terminal amino acid sequences of the four non-identical alpha chains of Rhodococcus sp.
A;Reference number: S03941; MUID:89231684; PMID:2496982
A;Accession: S03941
A;Molecule type: protein
A;Residues: 1-37 <ZAB>
A;Note: the source is designated as Nocardia opaca lb
C;Superfamily: hydrogen dehydrogenase alpha chain; NADH dehydrogenase (ubiquinone) I chain
C;Keywords: cytosol; oxidoreductase

Query Match 46.8%; Score 22; DB 2; Length 37;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 LMGYIP 7
: : |||
Db 28 LYGHIP 33

RESULT 36
A30010
cytochrome-c oxidase (EC 1.9.3.1) chain II homolog - Leishmania tarentolae mitochondrion
C;Species: mitochondrion Leishmania tarentolae
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 18-Aug-2003
C;Accession: A30010
R;de la Cruz, V.F.; Neckelmann, N.; Simpson, L.
J. Biol. Chem. 259, 15136-15147, 1984

A;Title: Sequences of six genes and several open reading frames in the kinetoplast maxicircle of *Leishmania tarentolae*

A;Reference number: A22848; MUID:85075995; PMID:6096360
 A;Accession: A30010
 A;Molecule type: DNA
 A;Residues: 1-42
 A;Cross-references: GB:M10126
 C;Genetics:
 A;Genome: mitochondrion
 A;Genetic code: SCS6
 C;Superfamily: cytochrome-c oxidase chain II, mitochondrial type; cytochrome-c oxidase c
 C;Keywords: copper; electron transfer; membrane-associated complex; mitochondrial inner

Query Match 46.8%; Score 22; DB 2; Length 42;
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LMGYIPAV 9
 |||
 Db 31 LMGFMPIV 38

RESULT 37
 PS0359
 hypothetical protein (VP16 3' region) - human herpesvirus 2 (fragment)
 C;Species: human herpesvirus 2
 C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Jul-2004
 C;Accession: PS0359
 R;Cress, A.; Trizzenberg, S.J.
 Gene 103, 235-238, 1991

A;Title: Nucleotide and deduced amino acid sequences of the gene encoding virion protein
 A;Reference number: J50689; MUID:91365250; PMID:1653757
 A;Accession: PS0359
 A;Molecule type: DNA
 A;Residues: 1-43 <CRE>
 A;Cross-references: UNIPROT:P89467; GB:M60050
 A;Experimental source: strain HG52
 C;Superfamily: herpesvirus 70.5K alpha trans-inducing protein

Query Match 46.8%; Score 22; DB 2; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LMGY 5
 |||
 Db 40 LMGY 43

RESULT 38
 C35156
 dihydroliipoamide dehydrogenase (EC 1.8.1.4) - *Peptostreptococcus glycinophilus* (fragment)
 C;Species: *Peptostreptococcus glycinophilus*
 C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 09-Jul-2004
 C;Accession: C35156
 R;Dietrichs, D.; Meyer, M.; Schmidt, B.; Andreesen, J.R.
 J. Bacteriol. 172, 2088-2095, 1990
 A;Title: Purification of NADPH-dependent electron-transferring flavoproteins and N-termi
 A;Reference number: A35156; MUID:90202731; PMID:2318809
 A;Accession: C35156
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-44 <DIE>

A;Cross-references: UNIPROT:Q7M0Y3
 C;Superfamily: dihydroliipoamide dehydrogenase; dihydroliipoamide dehydrogenase homology
 C;Keywords: FAD; flavoprotein; homodimer; lipoamide; NAD; oxidoreductase
 F;5-33/Region: beta-alpha-beta FAD nucleotide-binding fold

Query Match 46.8%; Score 22; DB 2; Length 44;
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GYIPAV 9
 |||
 Db 15 GYVAI 20

RESULT 39

B35156
 dihydroliipoamide dehydrogenase (EC 1.8.1.4) - *Clostridium sporogenes* (fragment)
 C;Species: *Clostridium sporogenes*
 C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 09-Jul-2004
 C;Accession: B35156
 R;Dietrichs, D.; Meyer, M.; Schmidt, B.; Andreesen, J.R.
 J. Bacteriol. 172, 2088-2095, 1990

A;Title: Purification of NADPH-dependent electron-transferring flavoproteins and N-termi
 A;Reference number: A35156; MUID:90202731; PMID:2318809
 A;Accession: B35156
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-45 <DIE>
 A;Cross-references: UNIPROT:Q7M0Y4
 C;Superfamily: dihydroliipoamide dehydrogenase; dihydroliipoamide dehydrogenase homology
 C;Keywords: FAD; flavoprotein; homodimer; lipoamide; NAD; oxidoreductase
 F;3-31/Region: beta-alpha-beta FAD nucleotide-binding fold

Query Match 46.8%; Score 22; DB 2; Length 45;
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GYIPAV 9
 |||
 Db 13 GYVAI 18

RESULT 40

S16924
 cytochrome cc3 - *Desulfovibrio vulgaris* (strain Miyazaki) (fragments)
 N;Alternate names: high-molecular-weight cytochrome c (HMW)
 C;Species: *Desulfovibrio vulgaris*
 C;Date: 19-Mar-1997 #sequence_revision 18-Jun-1999 #text_change 09-Jul-2004
 C;Accession: S16924
 R;Tasaka, C.; Ogata, M.; Yagi, T.; Tsugita, A.
 Protein Seq. Data Anal. 4, 25-27, 1991
 A;Title: Partial sequences of high-molecular-weight cytochrome c isolated from *Desulfovibrio*

A;Reference number: S16924; MUID:92020808; PMID:1656429
 A;Accession: S16924
 A;Molecule type: protein
 A;Residues: 1-30;31-48 <PRO>
 A;Cross-references: UNIPROT:Q7M0Z0
 A;Experimental source: strain Miyazaki
 C;Superfamily: cytochrome cc3; cytochrome c3 homology
 C;Keywords: blocked amino end; chromoprotein; heme; iron

Query Match 46.8%; Score 22; DB 2; Length 48;
 Best Local Similarity 57.1%; Pred. No. 1.7e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 MGYPVAV 9
 |||
 Db 30 VGTLPVAV 36

Search completed: August 23, 2005, 13:36:34
 Job time : 43 secs

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OM protein - protein search, using sw model

Run on: August 23, 2005, 13:35:09 ; Search time 158 Seconds
(without alignments)

22.306 Million cell updates/sec

Title: US-10-770-117-1

Perfect score: 47

Sequence: 1 DLMGYIPAV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 507806

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pdb.*
2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pdb.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pdb.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pdb.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pdb.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pdb.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pdb.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pdb.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pdb.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pdb.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pdb.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW PUB.pdb.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pdb.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pdb.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pdb.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pdb.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pdb.*
18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pdb.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pdb.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW PUB.pdb.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW PUB.pdb.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	9	14	US-10-114-823B-3
2	47	100.0	9	18	US-10-770-117-1
3	47	100.0	9	20	US-10-770-117-1
4	42	89.4	9	20	US-08-854-825-54
5	42	89.4	9	9	US-09-894-018-212
6	42	89.4	9	14	US-10-128-711-51
7	42	89.4	9	14	US-10-128-711-130
8	42	89.4	9	14	US-10-114-823B-20
9	42	89.4	9	15	US-10-371-525-255
10	42	89.4	9	15	US-10-371-069-255
11	42	89.4	9	15	US-10-371-645-255

9	15	US-10-371-260-255	Sequence 255, App
9	15	US-10-367-580-74	Sequence 74, Appl
9	15	US-10-367-593-74	Sequence 74, Appl
9	15	US-10-367-594-74	Sequence 74, Appl
9	15	US-10-367-654-74	Sequence 74, Appl
9	15	US-10-367-654-74	Sequence 74, Appl
9	15	US-10-367-658-74	Sequence 74, Appl
9	15	US-10-367-668-74	Sequence 74, Appl
9	16	US-10-440-390-2	Sequence 2, Appl
9	16	US-10-367-674-74	Sequence 74, Appl
9	16	US-10-777-053-199	Sequence 199, App
9	16	US-10-777-053-200	Sequence 200, App
9	16	US-10-777-053-426	Sequence 426, App
9	16	US-10-837-217-199	Sequence 199, App
9	16	US-10-837-217-200	Sequence 200, App
9	16	US-10-837-217-426	Sequence 426, App
9	16	US-10-474-960A-212	Sequence 212, App
9	18	US-10-481-696-19	Sequence 19, Appl
9	18	US-10-770-117-3	Sequence 3, Appl
9	20	US-11-082-595-20	Sequence 20, Appl
10	8	US-08-854-825-1	Sequence 1, Appl
10	16	US-10-777-053-109	Sequence 109, App
10	16	US-10-837-217-109	Sequence 109, App
10	17	US-10-931-566-26	Sequence 26, Appl
15	13	US-10-103-395-172	Sequence 172, App
15	14	US-10-268-561-14	Sequence 14, Appl
15	14	US-10-268-569-14	Sequence 14, Appl
20	9	US-09-894-018-4	Sequence 4, Appl
20	14	US-10-114-823B-2	Sequence 2, Appl
20	15	US-10-651-165-10	Sequence 10, Appl
20	16	US-10-474-960A-4	Sequence 4, Appl
20	20	US-11-082-595-2	Sequence 2, Appl
21	9	US-09-894-018-3	Sequence 3, Appl
21	16	US-10-474-960A-3	Sequence 3, Appl
22	14	US-10-296-558-7	Sequence 7, Appl
22	14	US-10-651-165-216	Sequence 216, App
24	15	US-09-891-983A-31	Sequence 31, Appl
25	10	US-09-891-983A-32	Sequence 32, Appl
25	14	US-10-173-480-58	Sequence 58, Appl
25	14	US-10-173-480-59	Sequence 59, Appl
25	16	US-10-753-910-58	Sequence 58, Appl
25	16	US-10-753-910-59	Sequence 59, Appl
30	15	US-10-296-734-424	Sequence 424, App
37	15	US-10-651-165-281	Sequence 281, App
8	9	US-09-989-621-10	Sequence 10, Appl
24	15	US-10-651-165-285	Sequence 285, App
8	15	US-10-651-165-69	Sequence 69, Appl
9	15	US-10-651-165-163	Sequence 163, App
10	15	US-10-367-593-75	Sequence 75, Appl
10	15	US-10-367-594-75	Sequence 75, Appl
10	15	US-10-367-654-75	Sequence 75, Appl
10	15	US-10-367-658-75	Sequence 75, Appl
10	15	US-10-367-668-75	Sequence 75, Appl
10	16	US-10-367-674-75	Sequence 75, Appl
10	16	US-10-777-053-108	Sequence 108, App
10	16	US-10-837-217-108	Sequence 108, App
20	15	US-10-651-165-11	Sequence 11, Appl
44	15	US-10-651-165-67	Sequence 67, Appl
28	14	US-10-109-670-45	Sequence 45, Appl
7	15	US-10-651-165-70	Sequence 70, Appl
30	15	US-10-296-734-426	Sequence 426, App
30	14	US-09-764-891-3423	Sequence 3423, App
30	14	US-10-091-573-301	Sequence 301, App
41	16	US-10-425-115-291449	Sequence 291449, App
41	16	US-10-425-115-291482	Sequence 291482, App
43	14	US-10-411-224-171	Sequence 171, App
43	15	US-10-047-021-171	Sequence 171, App
35	16	US-10-425-115-220432	Sequence 220432, App
38	14	US-10-029-386-31676	Sequence 31676, A
40	16	US-10-425-115-270620	Sequence 270620, App
43	16	US-10-425-115-256302	Sequence 256302, App
9	17	US-10-654-601-2277	Sequence 2277, App
10	9	US-09-766-412-20	Sequence 20, Appl

Sequence 232, App
 Sequence 284, App
 Sequence 284, App
 Sequence 284, App
 Sequence 284, App
 Sequence 232, App
 Sequence 9, Appl
 Sequence 10, Appl
 Sequence 1230, Ap
 Sequence 7, Appl
 Sequence 8, Appl
 Sequence 380, App
 Sequence 414, App
 Sequence 127, App
 Sequence 6, Appl
 Sequence 271139,

85 28 59.6 11 9 US-09-894-018-232
 86 28 59.6 11 15 US-10-371-525-284
 87 28 59.6 11 15 US-10-371-069-284
 88 28 59.6 11 15 US-10-371-645-284
 89 28 59.6 11 15 US-10-371-260-284
 90 28 59.6 11 16 US-10-474-960A-232
 91 28 59.6 12 17 US-10-777-893-9
 92 28 59.6 12 17 US-10-777-893-10
 93 28 59.6 14 17 US-10-813-638-1230
 94 28 59.6 14 17 US-10-925-556-7
 95 28 59.6 14 17 US-10-925-556-8
 96 28 59.6 20 14 US-10-280-066-380
 97 28 59.6 20 14 US-10-280-066-414
 98 28 59.6 23 14 US-10-078-090-127
 99 28 59.6 23 14 US-10-296-558-6
 100 28 59.6 30 15 US-10-424-599-271139

ALIGNMENTS

RESULT 1
 US-10-114-823B-3
 ; Sequence 3, Application US/10114823B
 ; Publication No. US20030099663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEITMANN, JULIA-KRISTINA
 ; APPLICANT: MATTNER, FRANK
 ; APPLICANT: BUSCHLE, MICHAEL
 ; APPLICANT: MELLING, JACK
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING AN ANTIGEN
 ; FILE REFERENCE: SONN:016US
 ; CURRENT APPLICATION NUMBER: US/10/114,823B
 ; CURRENT FILING DATE: 2002-04-01
 ; PRIOR APPLICATION NUMBER: PCT/EP00/09657
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: A-1680/99
 ; PRIOR FILING DATE: 1999-10-01
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 US-10-114-823B-3

Query Match 100.0%; Score 47; DB 14; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
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Db 1 DLMGYIPAV 9

RESULT 2
 US-10-770-117-1
 ; Sequence 1, Application US/10770117
 ; Publication No. US20050129705A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Government of the United States, as represented by the
 ; APPLICANT: Secretary, Dept. of
 ; APPLICANT: Health and Human Services
 ; APPLICANT: Berzofsky, Jay A.
 ; APPLICANT: Sarobe, Pablo
 ; APPLICANT: Pendleton, C. David
 ; APPLICANT: Feinstein, Stephen M.
 ; APPLICANT: Arichi, Tatsumi
 ; APPLICANT: Major, Marian E.
 ; TITLE OF INVENTION: MODIFIED HCV PEPTIDE VACCINES

FILE REFERENCE: 14014.0347/P
 ; CURRENT APPLICATION NUMBER: US/10/770,117
 ; CURRENT FILING DATE: 2004-02-02
 ; PRIOR APPLICATION NUMBER: US/09/763,260
 ; PRIOR FILING DATE: 2001-10-19
 ; PRIOR APPLICATION NUMBER: 60/097,446
 ; PRIOR FILING DATE: 1998-08-21
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Note =
 ; OTHER INFORMATION: synthetic construct
 US-10-770-117-1

Query Match 100.0%; Score 47; DB 18; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||

Db 1 DLMGYIPAV 9

RESULT 3
 US-11-082-595-3
 ; Sequence 3, Application US/11082595
 ; Publication No. US20050163797A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEITMANN, JULIA-KRISTINA
 ; APPLICANT: MATTNER, FRANK
 ; APPLICANT: BUSCHLE, MICHAEL
 ; APPLICANT: MELLING, JACK
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING AN ANTIGEN
 ; FILE REFERENCE: SONN:016US
 ; CURRENT APPLICATION NUMBER: US/11/082,595
 ; CURRENT FILING DATE: 2005-03-17
 ; PRIOR APPLICATION NUMBER: US/10/114,823
 ; PRIOR FILING DATE: 2002-04-01
 ; PRIOR APPLICATION NUMBER: PCT/EP00/09657
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: A-1680/99
 ; PRIOR FILING DATE: 1999-10-01
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 US-11-082-595-3

Query Match 100.0%; Score 47; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||

Db 1 DLMGYIPAV 9

RESULT 4
 US-08-854-825-54
 ; Sequence 54, Application US/08854825
 ; Publication No. US20020115061A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chisari, Francis V.
 ; APPLICANT: Cerny, Andreas


```

; TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T
; TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,825
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silver, Donald J.
; REGISTRATION NUMBER: 37552
; REFERENCE/DOCKET NUMBER: 61230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-854-825-54

Query Match 89.4%; Score 42; DB 8; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
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Db 1 DLMGYIPLV 9

RESULT 5
US-09-894-018-212
; Sequence 212, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 212
; LENGTH: 9
; TYPE: PRT

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; ORGANISM: Transgenic mouse
; US-09-894-018-212

Query Match 89.4%; Score 42; DB 9; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
   |||||
Db 1 DLMGYIPLV 9

RESULT 6
US-10-128-711-51
; Sequence 51, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-10-128-711-51

Query Match 89.4%; Score 42; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 1 DLMGYIPAV 9
| | | | | | |
Db 1 DLMGYIPLV 9

RESULT 7

US-10-128-711-130
; Sequence 130, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 130:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 130:
US-10-128-711-130

Query Match 89.4%; Score 42; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
| | | | | | |
Db 1 DLMGYIPLV 9

RESULT 8

US-10-114-823B-20

; Sequence 20, Application US/10114823B
; Publication No. US20030099663A1
; GENERAL INFORMATION:
; APPLICANT: FLEITMANN, JULIA-KRISTINA
; APPLICANT: MATTNER, FRANK
; APPLICANT: BUSCHLE, MICHAEL
; APPLICANT: MELLING, JACK
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING AN ANTIGEN
; FILE REFERENCE: SONN:016US
; CURRENT APPLICATION NUMBER: US/10/114,823B
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: PCT/EP00/09657
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: A-1680/99
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-114-823B-20

Query Match 89.4%; Score 42; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
| | | | | | |
Db 1 DLMGYIPLV 9

RESULT 9

US-10-371-525-255
; Sequence 255, Application US/10371525
; Publication No. US20030203869A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; IMMUNE RESPONSE AND METHODS OF USING THE SAME
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/10/371,525
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/311,784
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 255
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV Core 132 (peptide 1013.1002)
US-10-371-525-255

Query Match 89.4%; Score 42; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
| | | | | | |
Db 1 DLMGYIPLV 9

RESULT 10
US-10-371-069-255
; Sequence 255, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 255
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV Core 132 (peptide 1013.1002)
US-10-371-069-255

Query Match 89.4%; Score 42; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
| | | | | | | |
Db 1 DLMGYIPLV 9

RESULT 11
US-10-371-645-255
; Sequence 255, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 255
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV Core 132 (peptide 1013.1002)

US-10-371-645-255

Query Match 89.4%; Score 42; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
| | | | | | | |
Db 1 DLMGYIPLV 9

RESULT 12
US-10-371-260-255
; Sequence 255, Application US/10371260
; Publication No. US20030220285A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.13
; CURRENT APPLICATION NUMBER: US/10/371,260
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 255
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV Core 132 (peptide 1013.1002)
US-10-371-260-255

Query Match 89.4%; Score 42; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
| | | | | | | |
Db 1 DLMGYIPLV 9

RESULT 13
US-10-367-580-74
; Sequence 74, Application US/10367580
; Publication No. US20040071720A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461061
; CURRENT APPLICATION NUMBER: US/10/367,580
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,832
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16

```

; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 74
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-590-74

```

```

Query Match      89.4%; Score 42; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 DLMGYIPAV 9
   |||||
Db 1 DLMGYIPLV 9

```

```

RESULT 14
US-10-367-593-74
; Sequence 74, Application US/10367593
; Publication No. US20040071721A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461012
; CURRENT APPLICATION NUMBER: US/10/367,593
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 74
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-593-74

```

```

Query Match      89.4%; Score 42; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 DLMGYIPAV 9
   |||||
Db 1 DLMGYIPLV 9

```

```

RESULT 15
US-10-367-594-74
; Sequence 74, Application US/10367594
; Publication No. US20040071721A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.

```

```

; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461041
; CURRENT APPLICATION NUMBER: US/10/367,594
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/680,806
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 74
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-594-74

```

```

Query Match      89.4%; Score 42; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 DLMGYIPAV 9
   |||||
Db 1 DLMGYIPLV 9

```

```

RESULT 16
US-10-367-654-74
; Sequence 74, Application US/10367654
; Publication No. US20040071723A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461032
; CURRENT APPLICATION NUMBER: US/10/367,654
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 10/171,734
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/636,295
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 74
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-654-74

```

```
Query Match      89.4%; Score 42; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
      |||||
Db      1 DLMGYIPLV 9

RESULT 17
US-10-367-658-74
; Sequence 74, Application US/10367658
; Publication No. US20040071724A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461051
; CURRENT APPLICATION NUMBER: US/10/367,658
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,529
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 74
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-658-74

Query Match      89.4%; Score 42; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
      |||||
Db      1 DLMGYIPLV 9

RESULT 18
US-10-367-668-74
; Sequence 74, Application US/10367668
; Publication No. US20040071725A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461072
; CURRENT APPLICATION NUMBER: US/10/367,668
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,517
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
```

```
Query Match      89.4%; Score 42; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
      |||||
Db      1 DLMGYIPLV 9

RESULT 19
US-10-440-390-2
; Sequence 2, Application US/10440390
; Publication No. US20040105868A1
; GENERAL INFORMATION:
; APPLICANT: Lauer et al.
; TITLE OF INVENTION: Epitopes of Hepatitis C Virus
; FILE REFERENCE: 24028-011
; CURRENT APPLICATION NUMBER: US/10/440,390
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: 60/381,273
; PRIOR FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; OTHER INFORMATION: synthetic peptide
US-10-440-390-2

Query Match      89.4%; Score 42; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
      |||||
Db      1 DLMGYIPLV 9

RESULT 20
US-10-367-674-74
; Sequence 74, Application US/10367674
; Publication No. US20040127684A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/4610211
; CURRENT APPLICATION NUMBER: US/10/367,674
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 10/170,738
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/552,868
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 09/011,645
```

```
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 74
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-674-74

Query Match      89.4%; Score 42; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
Db      1 DLMGYIPLV 9

RESULT 21
US-10-777-053-199
; Sequence 199, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Cytomegalovirus
US-10-777-053-199

Query Match      89.4%; Score 42; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
Db      1 DLMGYIPLV 9

RESULT 22
US-10-777-053-200
; Sequence 200, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis C Virus
US-10-777-053-426

Query Match      89.4%; Score 42; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
Db      1 DLMGYIPLV 9

RESULT 23
US-10-777-053-426
; Sequence 426, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 426
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis C Virus
US-10-777-053-426

Query Match      89.4%; Score 42; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
Db      1 DLMGYIPLV 9

RESULT 24
US-10-837-217-199
; Sequence 199, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANNK.022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
```

Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
89.4%	88.9%	89.4%	42	16	0	0	0
8; Conservative	8; Conservative	0			1		
1 DLMGYIPAV 9	1 DLMGYIPAV 9						
1 DLMGYIPLV 9	1 DLMGYIPLV 9						
RESULT 27	US-10-474-960A-212						
Sequence 212, Application US/10474960A	Publication No. US20040248113A1						
GENERAL INFORMATION:							
APPLICANT: Sette, Alessandro							
APPLICANT: Chesnut, Robert							
APPLICANT: Livingston, Brian							
APPLICANT: Baker, Denise							
APPLICANT: Newman, Mark							
APPLICANT: Brown, David							
TITLE OF INVENTION: Methods and System for Optimizing Multi-epitope Nucleic							
TITLE OF INVENTION: Acid Constructs and Peptides Encoded Thereby							
FILE REFERENCE: 2060.0320004							
CURRENT APPLICATION NUMBER: US/10/474,960A							
CURRENT FILING DATE: 2003-10-16							
PRIOR APPLICATION NUMBER: PCT/US02/09877							
PRIOR FILING DATE: 2002-03-28							
PRIOR APPLICATION NUMBER: US 09/894,018							
PRIOR FILING DATE: 2001-06-27							
PRIOR APPLICATION NUMBER: US 60/284,221							
PRIOR FILING DATE: 2001-04-16							
NUMBER OF SEQ ID NOS: 419							
SOFTWARE: FastSeq for Windows Version 4.0							
SEQ ID NO 212							
LENGTH: 9							
TYPE: PRT							
ORGANISM: Artificial sequence							
FEATURE:							
OTHER INFORMATION: Sequence for epitope							
US-10-474-960A-212							
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
89.4%	88.9%	89.4%	42	16	0	0	0
8; Conservative	8; Conservative	0			1		
1 DLMGYIPAV 9	1 DLMGYIPAV 9						
1 DLMGYIPLV 9	1 DLMGYIPLV 9						
RESULT 28	US-10-481-696-19						
Sequence 19, Application US/10481696	Publication No. US20050129617A1						
GENERAL INFORMATION:							
APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA							
TITLE OF INVENTION: TYPE 1 DIABETES DIAGNOSTICS AND THERAPEUTICS							
FILE REFERENCE: 80021-365							
CURRENT APPLICATION NUMBER: US/10/481,696							
CURRENT FILING DATE: 2003-12-22							
PRIOR APPLICATION NUMBER: US 60/299,754							
PRIOR FILING DATE: 2001-06-22							
NUMBER OF SEQ ID NOS: 21							
SOFTWARE: PatentIn version 3.1							
SEQ ID NO 19							

```
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV peptide epitope
US-10-481-696-19

Query Match      89.4%; Score 42; DB 18; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 1 DLMGYIPLV 9
|||||||

RESULT 29
US-10-770-117-3
; Sequence 3, Application US/10770117
; Publication No. US20050129705A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States, as represented by the
; SECRETARY: Secretary, Dept. of
; APPLICANT: Health and Human Services
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Sarobe, Fabio
; APPLICANT: Pendleton, C. David
; APPLICANT: Feinstein, Stephen M.
; APPLICANT: Arichi, Tatsumi
; APPLICANT: Major, Marian E.
; TITLE OF INVENTION: MODIFIED HCV PEPTIDE VACCINES
; FILE REFERENCE: 14014.0347/P
; CURRENT APPLICATION NUMBER: US/10770,117
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: US/09/763,260
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/097,446
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./Note =
; OTHER INFORMATION: synthetic construct
US-10-770-117-3

Query Match      89.4%; Score 42; DB 18; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 1 DLMGYIPLV 9
|||||||

RESULT 30
US-11-082-595-20
; Sequence 20, Application US/11082595
; Publication No. US20050163797A1
; GENERAL INFORMATION:
; APPLICANT: FLEITMANN, JULIA-KRISTINA
; APPLICANT: MATTHEW, FRANK
; APPLICANT: BUSCHLE, MICHAEL
; APPLICANT: MELLING, JACK
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING AN ANTIGEN
; FILE REFERENCE: SONN:016US
; CURRENT APPLICATION NUMBER: US/11/082,595
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US/10/114,823
; PRIOR FILING DATE: 2002-04-01
```

```
; PRIOR APPLICATION NUMBER: PCT/EP00/09657
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: A-1680/99
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-082-595-20

Query Match      89.4%; Score 42; DB 20; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 1 DLMGYIPLV 9
|||||||

RESULT 31
US-08-854-825-1
; Sequence 1, Application US/08854825
; Publication No. US20020115061A1
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; APPLICANT: Cerny, Andreas
; TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T
; TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,825
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silver, Donald J.
; REGISTRATION NUMBER: 37552
; REFERENCE/DOCKET NUMBER: 61230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-854-825-1

Query Match      89.4%; Score 42; DB 8; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.23;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
|||||||
```



```
Db      2 DLMGYIPLV 10

RESULT 32
US-10-777-053-109
; Sequence 109, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Hepatitis C Virus
US-10-777-053-109

Query Match      89.4%; Score 42; DB 16; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.23;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
      |||||
Db      2 DLMGYIPLV 10

RESULT 33
US-10-837-217-109
; Sequence 109, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANK.022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Hepatitis C Virus
US-10-837-217-109

Query Match      89.4%; Score 42; DB 16; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.23;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
      |||||
Db      2 DLMGYIPLV 10

RESULT 34
US-10-931-566-26
; Sequence 26, Application US/10931566
; Publication No. US20050106137A1
; GENERAL INFORMATION:
; APPLICANT: Apton Corporation
; APPLICANT: Grimes, Stephen
; TITLE OF INVENTION: Chimeric Peptide Immunogens
; FILE REFERENCE: 1102865-0047CIP
; CURRENT APPLICATION NUMBER: US/10/931,566
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: 09/848,834
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,328
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-931-566-26

Query Match      89.4%; Score 42; DB 17; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.23;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
      |||||
Db      2 DLMGYIPLV 10

RESULT 35
US-10-103-395-172
; Sequence 172, Application US/10103395
; Publication No. US20020160019A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
; TITLE OF INVENTION: RESTRICTED EPITOPES
; FILE REFERENCE: 39963-20016.01
; CURRENT APPLICATION NUMBER: US/10/103,395
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 09/009,953
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: PCT/US98/01373
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: US 60/036,713
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 60/037,432
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 172
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-395-172

Query Match      89.4%; Score 42; DB 13; Length 15;
Best Local Similarity 88.9%; Pred. No. 0.35;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
      |||||
Db      2 DLMGYIPLV 10

RESULT 36
US-10-268-561-14
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;
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
;
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; APPLICANT: MARIENS, GUELL
; TITLE OF INVENTION: VIRUS

```

```

; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-10

Query Match      89.4%; Score 42; DB 15; Length 20;
Best Local Similarity 88.9%; Pred. No. 0.47;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
        |||||
Db      12 DLMGYIPLV 20

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Search completed: August 23, 2005, 13:48:40
Job time : 160 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 13:23:38 : Search time 41 Seconds
(without alignments)

16.386 Million cell updates/sec

Title: US-10-770-117-1

Perfect score: 47

Sequence: 1 DLMGYIPAV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 272444

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
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5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	9	4	US-09-763-260-1
2	42	89.4	9	1	US-08-214-650-54
3	42	89.4	9	4	US-08-197-484-51
4	42	89.4	9	4	US-08-197-484-51
5	42	89.4	9	4	US-08-197-484-130
6	42	89.4	9	4	US-09-311-784A-255
7	42	89.4	9	4	US-09-763-260-3
8	42	89.4	9	5	PCT-US95-02121-51
9	42	89.4	10	1	US-08-214-650-1
10	42	89.4	15	4	US-09-009-953-172
11	42	89.4	16	2	US-08-986-234-34
12	42	89.4	20	4	US-08-635-886C-10
13	42	89.4	20	4	US-08-974-690C-10
14	42	89.4	20	4	US-08-974-685-10
15	42	89.4	24	4	US-08-635-886C-216
16	42	89.4	24	4	US-08-974-690C-216
17	42	89.4	25	4	US-10-173-480-58
18	42	89.4	25	4	US-10-173-480-59
19	42	89.4	37	4	US-08-635-886C-281
20	42	89.4	37	4	US-08-974-690C-281
21	39	83.0	8	3	US-09-051-006-10
22	38	80.9	24	4	US-08-635-886C-285
23	38	80.9	24	4	US-08-974-690C-285
24	36	76.6	8	4	US-08-635-886C-69
25	36	76.6	8	4	US-08-974-690C-69
26	36	76.6	8	4	US-08-974-685-69
27	36	76.6	9	4	US-08-635-886C-163

28	36	76.6	9	4	US-08-974-690C-163
29	36	76.6	9	4	US-08-974-685-163
30	36	76.6	10	2	US-08-986-234-35
31	36	76.6	20	4	US-08-635-886C-11
32	36	76.6	20	4	US-08-974-690C-11
33	36	76.6	20	4	US-08-974-685-11
34	36	76.6	44	4	US-08-635-886C-67
35	36	76.6	44	4	US-08-974-690C-67
36	36	76.6	44	4	US-08-974-685-67
37	35	74.5	23	1	US-08-189-331-179
38	35	74.5	23	2	US-08-471-068-179
39	33	70.2	28	4	US-09-091-097-45
40	32	68.1	7	4	US-08-635-886C-70
41	32	68.1	7	4	US-08-974-690C-70
42	32	68.1	7	4	US-08-974-685-70
43	31	66.0	20	1	US-07-678-974D-61
44	31	66.0	20	2	US-08-945-168-67
45	31	66.0	50	4	US-09-621-976-5926
46	29	61.7	24	4	US-08-492-723-3
47	28	59.6	9	4	US-09-239-043D-2277
48	28	59.6	10	3	US-09-385-442-20
49	28	59.6	11	4	US-09-311-784A-284
50	28	59.6	15	2	US-08-480-473B-15
51	28	59.6	15	3	US-08-915-213-15
52	28	59.6	15	3	US-09-235-217-15
53	28	59.6	15	5	PCT-US96-10251-15
54	28	59.6	20	1	US-07-678-974D-62
55	28	59.6	20	2	US-08-945-168-68
56	28	59.6	23	1	US-08-582-257-2
57	28	59.6	23	2	US-08-582-298-2
58	27	57.4	46	4	US-09-079-030-18
59	27	57.4	50	3	US-08-938-830-5
60	27	57.4	50	3	US-09-020-223-5
61	26	55.3	15	4	US-09-009-953-176
62	26	55.3	16	4	US-08-635-886C-61
63	26	55.3	16	4	US-08-974-690C-61
64	26	55.3	16	4	US-08-974-685-61
65	26	55.3	16	4	US-08-974-685-62
66	26	55.3	20	4	US-09-790-497A-446
67	26	55.3	20	4	US-09-576-824A-446
68	26	55.3	20	4	US-09-413-564C-35
69	26	55.3	20	4	US-09-413-564C-36
70	26	55.3	20	4	US-09-413-564C-37
71	26	55.3	27	4	US-09-413-564C-34
72	26	55.3	45	6	5177197-47
73	26	55.3	45	6	5177197-47
74	26	55.3	47	4	US-08-826-134-14
75	26	55.3	47	4	US-08-826-134-25
76	26	55.3	50	4	US-09-270-767-37069
77	26	55.3	50	4	US-09-270-767-52286
78	25	53.2	10	1	US-07-841-662-24
79	25	53.2	10	1	US-08-209-797-24
80	25	53.2	10	2	US-08-669-685-24
81	25	53.2	10	3	US-09-103-486-24
82	25	53.2	10	3	US-09-385-442-2
83	25	53.2	10	3	US-09-039-982A-40
84	25	53.2	10	3	US-09-039-641-40
85	25	53.2	10	3	US-09-039-762A-40
86	25	53.2	10	3	US-09-042-492D-40
87	25	53.2	10	4	US-08-913-612A-40
88	25	53.2	10	4	US-10-266-463A-40
89	25	53.2	10	5	PCT-US93-01557-24
90	25	53.2	11	3	US-09-298-924-34
91	25	53.2	13	2	US-08-210-421-1
92	25	53.2	13	3	US-08-704-727-1
93	25	53.2	13	4	US-09-412-420-1
94	25	53.2	13	5	PCT-US95-03311-1
95	25	53.2	20	1	US-08-399-646-9
96	25	53.2	20	1	US-08-607-321-9
97	25	53.2	20	2	US-08-961-240-9
98	25	53.2	20	2	US-08-605-501-9
99	25	53.2	25	1	US-08-433-854-10
100	25	53.2	25	1	US-08-174-745A-10

Sequence 163, App
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Sequence 35, App
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Sequence 179, App
Sequence 45, Appl
Sequence 70, Appl
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Sequence 61, Appl
Sequence 5926, Ap
Sequence 3, Appl
Sequence 2277, Ap
Sequence 20, Appl
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Sequence 15, Appl
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Sequence 40, Appl
Sequence 34, Appl
Sequence 34, Appl
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Sequence 1, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 10, Appl
Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-763-260-1
; Sequence 1, Application US/09763260
; Patent No. 6685944
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States, as represented by the
; APPLICANT: Secretary, Dept. of
; APPLICANT: Health and Human Services
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Sarobe, Pablo
; APPLICANT: Pendleton, C. David
; APPLICANT: Feinstein, Stephen M.
; APPLICANT: Arichi, Tatsumi
; APPLICANT: Major, Marian E.
; TITLE OF INVENTION: MODIFIED HCV PEPTIDE VACCINES
; FILE REFERENCE: 14014.0347/P
; CURRENT APPLICATION NUMBER: US/09/763,260
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/097,446
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. 6685944e =
; OTHER INFORMATION: synthetic construct
US-09-763-260-1

Query Match 100.0%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 1 DLMGYIPAV 9

RESULT 2

US-08-214-650-54
; Sequence 54, Application US/08214650
; Patent No. 5703995
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; APPLICANT: Cerny, Andreas
; TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T
; TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,650
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Silver, Donald J.

; REGISTRATION NUMBER: 37552
; REFERENCE/DOCKET NUMBER: 61230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-214-650-54
Query Match 89.4%; Score 42; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DLMGYIPAV 9
Db 1 DLMGYIPLV 9
RESULT 3
US-08-197-484-51
; Sequence 51, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Eteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-197-484-51

Query Match 89.4%; Score 42; DB 4; Length 9;
 Best Local Similarity 88.9%; Pred. No. 4.1e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
 Db 1 DLMGYIPLV 9

RESULT 4
 US-08-197-484-130
 ; Sequence 130, Application US/08197484
 ; Patent No. 6419331
 ; GENERAL INFORMATION:
 ; APPLICANT: VITIELLO, Maria A.
 ; APPLICANT: CHESTNUT, Robert W.
 ; APPLICANT: SETTE, Alessandro D.
 ; APPLICANT: CELIS, Esteban
 ; APPLICANT: GRAY, Howard
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
 ; TITLE OF INVENTION: CTL IMMUNITY
 ; NUMBER OF SEQUENCES: 153
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: Steuart Street Tower, One Market Plaza
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94105-1493

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/197,484
 FILING DATE: 16-FEB-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/935,811
 FILING DATE: 26-AUG-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/874,491
 FILING DATE: 27-APR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,682
 FILING DATE: 29-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/749,568
 FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:
 NAME: Parmelee, Steven W.
 REGISTRATION NUMBER: 31,990
 REFERENCE/DOCKET NUMBER: 14137-26-4
 TELEPHONE: (206) 467-9600
 TELEFAX: (206) 623-6793
 INFORMATION FOR SEQ ID NO: 130:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-197-484-130

Query Match 89.4%; Score 42; DB 4; Length 9;
 Best Local Similarity 88.9%; Pred. No. 4.1e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
 Db 1 DLMGYIPLV 9

RESULT 5
 US-09-311-784A-255
 ; Sequence 255, Application US/09311784A
 ; Patent No. 6534482
 ; GENERAL INFORMATION:
 ; APPLICANT: Fikes, John D.
 ; APPLICANT: Hermanson, Gary G.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Ishioka, Glenn Y.
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Chesnut, Robert W.
 ; APPLICANT: Epimmune Inc.
 ; TITLE OF INVENTION: Expression Vectors for Stimulating an
 ; TITLE OF INVENTION: Immune Response and Methods of Using the Same
 ; FILE REFERENCE: 39963-20022.01
 ; CURRENT APPLICATION NUMBER: US/09/311,784A
 ; CURRENT FILING DATE: 1999-05-13
 ; PRIOR APPLICATION NUMBER: US 60/085,751
 ; PRIOR FILING DATE: 1998-05-15
 ; NUMBER OF SEQ ID NOS: 463
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 255
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: HCV Core 132 (peptide 1013.1002)
 US-09-311-784A-255

Query Match 89.4%; Score 42; DB 4; Length 9;
 Best Local Similarity 88.9%; Pred. No. 4.1e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
 Db 1 DLMGYIPLV 9

RESULT 6
 US-09-763-260-3
 ; Sequence 3, Application US/09763260
 ; Patent No. 6685944
 ; GENERAL INFORMATION:
 ; APPLICANT: The Government of the United States, as represented by the
 ; APPLICANT: Secretary, Dept. of
 ; APPLICANT: Health and Human Services
 ; APPLICANT: Berzofsky, Jay A.
 ; APPLICANT: Sarobe, Pablo
 ; APPLICANT: Pendleton, C. David
 ; APPLICANT: Feinstein, Stephen M.
 ; APPLICANT: Arichi, Tatsumi
 ; APPLICANT: Major, Marian E.
 ; TITLE OF INVENTION: MODIFIED HCV PEPTIDE VACCINES
 ; FILE REFERENCE: 14014.0347/P
 ; CURRENT APPLICATION NUMBER: US/09/763,260
 ; CURRENT FILING DATE: 2001-10-19
 ; PRIOR APPLICATION NUMBER: 60/097,446
 ; PRIOR FILING DATE: 1998-08-21
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 9
 ; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./No. 6685944e =
US-09-763-260-3
    Query Match      89.4%; Score 42; DB 4; Length 9;
    Best Local Similarity 88.9%; Pred. No. 4.1e+05;
    Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
        |||||
Db      1 DLMGYIPLV 9

RESULT 7
PCT-US95-02121-51
; Sequence 51, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-51

    Query Match      89.4%; Score 42; DB 5; Length 9;
    Best Local Similarity 88.9%; Pred. No. 4.1e+05;
    Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
        |||||
Db      1 DLMGYIPLV 9

RESULT 8
PCT-US95-02121-51
; Sequence 51, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-51

    Query Match      89.4%; Score 42; DB 5; Length 9;
    Best Local Similarity 88.9%; Pred. No. 4.1e+05;
    Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
        |||||
Db      1 DLMGYIPLV 9

RESULT 9
US-08-214-650-1
; Sequence 1, Application US/08214650
; Patent No. 5709995
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; APPLICANT: Cerny, Andreas
; TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T
; TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voigt & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
```

```
PCT-US95-02121-130
; Sequence 130, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 130:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-130

    Query Match      89.4%; Score 42; DB 5; Length 9;
    Best Local Similarity 88.9%; Pred. No. 4.1e+05;
    Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
        |||||
Db      1 DLMGYIPLV 9

RESULT 9
US-08-214-650-1
; Sequence 1, Application US/08214650
; Patent No. 5709995
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; APPLICANT: Cerny, Andreas
; TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T
; TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voigt & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
```


COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/214,650
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Silver, Donald J.
REGISTRATION NUMBER: 37552
REFERENCE/DOCKET NUMBER: 61230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-214-650-1

Query Match 89.4%; Score 42; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.023;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 2 DLMGYIPLV 10
|||||

RESULT 10
US-09-009-953-172
Sequence 172, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-Jan-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 172:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 172:
US-09-009-953-172

Query Match 89.4%; Score 42; DB 4; Length 15;
Best Local Similarity 88.9%; Pred. No. 0.036;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 2 DLMGYIPLV 10
|||||

RESULT 11
US-08-986-234-34
Sequence 34, Application US/08986234
Patent No. 5981706
GENERAL INFORMATION:
APPLICANT: Wallen, et al.
TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Complexes
FILE REFERENCE: UNME-0008-1
CURRENT APPLICATION NUMBER: US/08/986,234
CURRENT FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 16
TYPE: PRT
ORGANISM: Hepatitis C virus
US-08-986-234-34

Query Match 89.4%; Score 42; DB 2; Length 16;
Best Local Similarity 88.9%; Pred. No. 0.039;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 4 DLMGYIPLV 12
|||||

RESULT 12
US-08-635-886C-10
Sequence 10, Application US/08635886C
Patent No. 6555114
GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: MAERTENS, Geert
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
FILE REFERENCE: 2752-18
CURRENT APPLICATION NUMBER: US/08/635,886C
CURRENT FILING DATE: 1996-04-25
PRIOR APPLICATION NUMBER: PCT/EP94/03555
PRIOR FILING DATE: 1994-10-28
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 20
TYPE: PRT
ORGANISM: hepatitis C virus
US-08-635-886C-10

Query Match 89.4%; Score 42; DB 4; Length 20;
Best Local Similarity 88.9%; Pred. No. 0.05;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
| | | | | | | |
Db 12 DLMGYIPLV 20

RESULT 13
US-08-974-690C-10
; Sequence 10, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-10

Query Match 89.4%; Score 42; DB 4; Length 20;
Best Local Similarity 88.9%; Pred. No. 0.05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
| | | | | | | |
Db 12 DLMGYIPLV 20

RESULT 14
US-08-974-685-10
; Sequence 10, Application US/08974685
; Patent No. 6689368
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, GEERT
; APPLICANT: DELEYS, ROBERT
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF
HEPATITIS C VIRUS STRUCTURAL PROTEINS, PROPHYLACTIC AND
THERAPEUTIC COMPOSITIONS CONTAINING THE SAME

NUMBER OF SEQUENCES: 181
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,685
FILING DATE: 19-NOV-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-11

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-08-974-685-10

Query Match 89.4%; Score 42; DB 4; Length 20;
Best Local Similarity 88.9%; Pred. No. 0.05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
| | | | | | | |
Db 12 DLMGYIPLV 20

RESULT 15
US-08-635-886C-216
; Sequence 216, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 216
; LENGTH: 24
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-216

Query Match 89.4%; Score 42; DB 4; Length 24;
Best Local Similarity 88.9%; Pred. No. 0.062;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
| | | | | | | |
Db 6 DLMGYIPLV 14

RESULT 16
US-08-974-690C-216
; Sequence 216, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04

Tue Aug 23 14:25:42 2005

; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 216
; LENGTH: 24
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-216

Query Match 89.4%; Score 42; DB 4; Length 24;
Best Local Similarity 88.9%; Pred. No. 0.062;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | | | | |
Db 6 DLMGYIPLV 14

RESULT 17
US-10-173-480-58
; Sequence 58, Application US/10173480
; Patent No. 6727092

; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Shah, Dinesh O.
; APPLICANT: Dawson, George A.
; APPLICANT: Muerhoff, A. Scott
; APPLICANT: Jiang, Lily
; APPLICANT: Gutierrez, Robin A.
; APPLICANT: Leary, Thomas P.
; APPLICANT: Desai, Suresh
; APPLICANT: Stewart, James L.
; TITLE OF INVENTION: METHODS FOR THE SIMULTANEOUS DETECTION
; OF HCV ANTIGENS AND HCV ANTIBODIES
; FILE REFERENCE: 6821.US.P1
; CURRENT APPLICATION NUMBER: US/10/173,480
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/891,983
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV-Core derived peptides
US-10-173-480-58

Query Match 89.4%; Score 42; DB 4; Length 25;
Best Local Similarity 88.9%; Pred. No. 0.065;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | | | | |
Db 17 DLMGYIPLV 25

RESULT 18
US-10-173-480-59
; Sequence 59, Application US/10173480
; Patent No. 6727092

; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Shah, Dinesh O.
; APPLICANT: Dawson, George A.
; APPLICANT: Muerhoff, A. Scott
; APPLICANT: Jiang, Lily
; APPLICANT: Gutierrez, Robin A.
; APPLICANT: Leary, Thomas P.
; APPLICANT: Desai, Suresh
; APPLICANT: Stewart, James L.
; TITLE OF INVENTION: METHODS FOR THE SIMULTANEOUS DETECTION
; OF HCV ANTIGENS AND HCV ANTIBODIES

; FILE REFERENCE: 6821.US.P1
; CURRENT APPLICATION NUMBER: US/10/173,480
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/891,983
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV-Core derived peptides
US-10-173-480-59

Query Match 89.4%; Score 42; DB 4; Length 25;
Best Local Similarity 88.9%; Pred. No. 0.065;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | | | | |
Db 7 DLMGYIPLV 15

RESULT 19
US-08-635-886C-281
; Sequence 281, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 281
; LENGTH: 37
; TYPE: PRT
; ORGANISM: hepatitis C virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (28)..(29)
; OTHER INFORMATION: Xaa is any amino acid
US-08-635-886C-281

Query Match 89.4%; Score 42; DB 4; Length 37;
Best Local Similarity 88.9%; Pred. No. 0.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | | | | |
Db 19 DLMGYIPLV 27

RESULT 20
US-08-974-690C-281
; Sequence 281, Application US/08974690C

```

; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 281
; LENGTH: 37
; TYPE: PRT
; ORGANISM: hepatitis C virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (28)..(29)
; OTHER INFORMATION: Xaa is any amino acid
; US-08-974-690C-281

Query Match      89.4%; Score 42; DB 4; Length 37;
Best Local Similarity 89.9%; Pred. No. 0.1;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

Qy      1 DLMGYIPAV 9
Db      19 DLMGYIPLV 27

RESULT 21
US-09-051-006-10
; Sequence 10, Application US/09051006
; Patent No. 6380359
; GENERAL INFORMATION:
; APPLICANT: Mogam Biotechnology Research Institute
; APPLICANT: Kim, Tae-Young
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Myeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; TITLE OF INVENTION: Derived from X Protein of Hepatitis B virus
; FILE REFERENCE: 0136/OE154
; CURRENT APPLICATION NUMBER: US/09/051,006
; CURRENT FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HCV
; US-09-051-006-10

Query Match      83.0%; Score 39; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 DLMGYIP 7
Db      1 DLMGYIP 7

RESULT 22
US-08-635-886C-285
; Sequence 285, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 285
; LENGTH: 24
; TYPE: PRT
; ORGANISM: hepatitis C virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (3)..(4)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (11)..(11)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (21)..(21)
; OTHER INFORMATION: Xaa is any amino acid
; US-08-635-886C-285

Query Match      80.9%; Score 38; DB 4; Length 24;
Best Local Similarity 77.8%; Pred. No. 0.41;
Matches      7; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

Qy      1 DLMGYIPAV 9
Db      6 DLMGYXPVV 14

RESULT 23
US-08-974-690C-285
; Sequence 285, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 285
; LENGTH: 24
; TYPE: PRT
```

; ORGANISM: hepatitis C virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (3)..(4)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (11)..(11)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (21)..(21)
; OTHER INFORMATION: Xaa is any amino acid
US-08-974-690C-285

Query Match 80.9%; Score 38; DB 4; Length 24;
Best Local Similarity 77.8%; Pred. No. 0.41;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DLMGVIPAV 9
| | | | | | | |
Db 6 DLMGYXPV 14

RESULT 24
US-08-635-886C-69
; Sequence 69, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; PRIORITY FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 8
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-69

Query Match 76.6%; Score 36; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LMGVIPAV 9
| | | | | | | |
Db 1 LMGYIPLV 8

RESULT 25
US-08-974-690C-69
; Sequence 69, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28

; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 8
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-69

Query Match 76.6%; Score 36; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LMGVIPAV 9
| | | | | | | |
Db 1 LMGYIPLV 8

RESULT 26
US-08-974-685-69
; Sequence 69, Application US/08974685
; Patent No. 668368
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, GEERT
; APPLICANT: DELEYS, ROBERT
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF
HEPATITIS C VIRUS STRUCTURAL PROTEINS, PROPHYLACTIC AND
THERAPEUTIC COMPOSITIONS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
; COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,685
FILING DATE: 19-NOV-97
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 69:

Query Match 76.6%; Score 36; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LMGVIPAV 9
| | | | | | | |
Db 1 LMGYIPLV 8

```
RESULT 27
US-08-635-886C-163
; Sequence 163, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2752-18
; CURRENT FILING DATE: 1996-04-25
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-163

Query Match      76.6%; Score 36; DB 4; Length 9;
Best Local Similarity 87.5%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LMGYIPAV 9
      |||||
Db      2 LMGYIPLV 9

RESULT 28
US-08-974-690C-163
; Sequence 163, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-163

Query Match      76.6%; Score 36; DB 4; Length 9;
Best Local Similarity 87.5%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LMGYIPAV 9
      |||||
Db      2 LMGYIPLV 9

RESULT 29
US-08-974-685-163
; Sequence 163, Application US/08974685
; Patent No. 6689368
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, GEERT
; DELEYS, ROBERT
; MAERTENS, GEERT
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF
; HEPATITIS C VIRUS STRUCTURAL PROTEINS, PROPHYLACTIC AND
; THERAPEUTIC COMPOSITIONS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,685
; FILING DATE: 19-NO. 6689368-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 163:
US-08-974-685-163

Query Match      76.6%; Score 36; DB 4; Length 9;
Best Local Similarity 87.5%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LMGYIPAV 9
      |||||
Db      2 LMGYIPLV 9

RESULT 30
US-08-986-234-35
; Sequence 35, Application US/08986234
; Patent No. 5981706
; GENERAL INFORMATION:
; APPLICANT: Wallen, et al.
; TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Complexes
; FILE REFERENCE: UNME-0008-1
; CURRENT APPLICATION NUMBER: US/08/986,234
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-08-986-234-35

Query Match      76.6%; Score 36; DB 2; Length 10;
Best Local Similarity 87.5%; Pred. No. 0.4;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LMGYIPAV 9
      |||||
Db      2 LMGYIPLV 9
```

```
Db      1 LMGVIPLV 8

RESULT 31
US-08-635-886C-11
; Sequence 11, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-11

Query Match      76.6%; Score 36; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 0.87;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy      2 LMGYIPAV 9
       |||||
Db      1 LMGVIPLV 8

RESULT 32
US-08-974-690C-11
; Sequence 11, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-11

Query Match      76.6%; Score 36; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 0.87;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy      2 LMGYIPAV 9
       |||||
Db      1 LMGVIPLV 8

RESULT 33
US-08-974-685-11
; Sequence 11, Application US/08974685
; Patent No. 6689368
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, GEERT
; APPLICANT: DELEYS, ROBERT
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF
; HEPATITIS C VIRUS STRUCTURAL PROTEINS, PROPHYLACTIC AND
; THERAPEUTIC COMPOSITIONS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,685
; FILING DATE: 19-NO. 6689368-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-974-685-11

Query Match      76.6%; Score 36; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 0.87;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy      2 LMGYIPAV 9
       |||||
Db      1 LMGVIPLV 8

RESULT 34
US-08-635-886C-67
; Sequence 67, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 67
; LENGTH: 44
```

```
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-67

Query Match      76.6%; Score 36; DB 4; Length 44;
Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LMGYIPAV 9
      |||||
Db      1 LMGYIPLV 8

RESULT 35
US-08-974-690C-67
; Sequence 67, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-67

Query Match      76.6%; Score 36; DB 4; Length 44;
Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LMGYIPAV 9
      |||||
Db      1 LMGYIPLV 8

RESULT 36
US-08-974-685-67
; Sequence 67, Application US/08974685
; Patent No. 6689368
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, GEERT
; APPLICANT: DELEYS, ROBERT
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF
; HEPATITIS C VIRUS STRUCTURAL PROTEINS, PROPHYLACTIC AND
; THERAPEUTIC COMPOSITIONS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,685
```

```
; FILING DATE: 19-No. 6689368-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-08-974-685-67

Query Match      76.6%; Score 36; DB 4; Length 44;
Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LMGYIPAV 9
      |||||
Db      1 LMGYIPLV 8

RESULT 37
US-08-189-331-179
; Sequence 179, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowlkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,331
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Miarock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIR
; INFORMATION FOR SEQ ID NO: 179:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-189-331-179

Query Match      74.5%; Score 35; DB 1; Length 23;
Best Local Similarity 75.0%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```


Qy 1 DLMGVIPA 8
Db 16 DLSGYLPA 23

RESULT 38
US-08-471-068-179
; Sequence 179, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowlkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471.068
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,331
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 179:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-068-179

Query Match 74.5%; Score 35; DB 2; Length 23;
Best Local Similarity 75.0%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGVIPA 8
Db 16 DLSGYLPA 23

RESULT 39
US-09-091-097-45
; Sequence 45, Application US/09091097
; Patent No. 6432407
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH
; APPLICANT: OKADO, TAKASHI
; APPLICANT: YAGIHARA, TOMOKO
; APPLICANT: KURODA, MASANOBU
; APPLICANT: ONISHI, YOSHIMI
; APPLICANT: KATO, IKUNOSHIN
; APPLICANT: AKIYAMA, KAZUO
; APPLICANT: YASUEDA, HIROSHI

; APPLICANT: YAMAGUCHI, HIDEYO
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,097
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0346P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-091-097-45

Query Match 70.2%; Score 33; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LMGVIP 7
Db 17 LMGVIP 22

RESULT 40
US-08-635-886C-70
; Sequence 70, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70
; LENGTH: 7
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-70

Query Match 68.1%; Score 32; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 MGYIPAV 9
| | | | |
Db 1 MGYIPLV 7

Search completed: August 23, 2005, 13:35:47
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 13:17:43 ; Search time 161 Seconds

(without alignments)
21.620 Million cell updates/sec

Title: US-10-770-117-1

Perfect score: 47

Sequence: 1 DLNGYIPAV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 938430

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	47	100.0	9	3 AAY82996	Aay82996 Substitut
2	47	100.0	9	4 AAB82052	Aab82052 HCV anti
3	43	91.5	15	8 ADL25899	Adl25899 Synthetic
4	43	91.5	15	8 ADL25904	Adl25904 Synthetic
5	43	91.5	15	8 ADL25905	Adl25905 Synthetic
6	43	91.5	15	8 ADL25900	Adl25900 Synthetic
7	43	91.5	15	8 ADL25901	Adl25901 Synthetic
8	43	91.5	15	8 ADL25903	Adl25903 Synthetic
9	43	91.5	15	8 ADL25902	Adl25902 Synthetic
10	43	91.5	36	8 ADL26466	Adl26466 Synthetic
11	42	89.4	9	2 AAR73111	Aar73111 Antigen f
12	42	89.4	9	2 AAR59125	Aar59125 Peptide f
13	42	89.4	9	2 AAR78946	Aar78946 HCV core
14	42	89.4	9	2 AAR87652	Aar87652 Hepatitis
15	42	89.4	9	2 AAR91054	Aar91054 HCV-1 der
16	42	89.4	9	2 AAW39446	Aaw39446 Human HCV
17	42	89.4	9	2 AAW54635	Aaw54635 Peptide f
18	42	89.4	9	2 AAY10219	Aay10219 T cell ep
19	42	89.4	9	3 AAY10441	Aay10441 HLA Class
20	42	89.4	9	3 AAY73106	Aay73106 Hepatitis
21	42	89.4	9	3 AAY82998	Aay82998 Hepatitis
22	42	89.4	9	4 AAJ03866	Aaj03866 Hepatitis
23	42	89.4	9	4 AAJ01746	Aaj01746 Hepatitis
24	42	89.4	9	4 AAJ03964	Aaj03964 Hepatitis
25	42	89.4	9	4 AAJ00011	Aaj00011 Hepatitis

AAJ00229 Hepatitis
AAJ03787 Hepatitis
AAJ04086 Hepatitis
ABG79901 MHC class
ABG80124 MHC class
ABP70576 Hepatitis
ADA49528 Multi-epi
ADE97587 Immunogen
ADK69063 CTL epitope
ADK68337 Epitope 1
ADK84718 Hepatitis
ADO24206 HCV epitope
ADO08619 Hepatitis
ADQ10635 Hepatitis
ADQ10634 Human her
ADQ10861 Hepatitis
ADR11676 HLA-A2.1
ADR69426 Novel hyb
ADR84570 Cytotoxic
AAW39445 Human HCV
AAY10135 T cell ep
ABG79818 MHC class
ADK68746 Epitope 1
ADQ10544 Hepatitis
AAJ01550 Hepatitis
AAJ00230 Hepatitis
AAJ01947 Hepatitis
AAJ02126 Hepatitis
AAJ00276 Hepatitis
AAW85270 Helper T-
AAJ03485 Hepatitis
AAJ03147 Hepatitis
AAJ03178 Hepatitis
AAJ03985 Hepatitis
ABR55585 Amino aci
ADH19101 HCV core
ADI34998 Hepatitis
ADI34999 Hepatitis
ADL25886 Synthetic
ADL25882 Synthetic
ADL25885 Synthetic
ADL25883 Synthetic
ADL25887 Synthetic
ADL25888 Synthetic
ADL25884 Synthetic
ADO23855 HBV pepti
AAR87651 Hepatitis
AAY25210 HCV viral
ABP70575 Hepatitis
AAR56611 HCV pepti
AAR56610 HCV pepti
AAR84500 Hepatitis
AAB82051 HCV anti
AAG64436 Hepatitis
ADA49671 Multi-epi
ADM23200 Hepatitis
ADO23856 HBV pepti
AAG64435 Hepatitis
ADA49670 Multi-epi
ABO4527 Hepatitis
ADI34954 Hepatitis
ABJ37519 HCV-core
ABJ37520 HCV-core
ADJ84719 Lipopepti
AAU84606 HCV HepC1
ADL26465 Synthetic
AAY24468 Hepatitis
AAJ01618 Hepatitis
AAJ00864 Hepatitis
AAJ00228 Hepatitis
ADN64405 HLA bindi
AAJ01478 Hepatitis

99 39 83.0 10 4 AAJ00275 Aaj00275 Hepatitis
100 39 83.0 11 4 AAJ02942 Aaj02942 Hepatitis

ALIGNMENTS

RESULT 1

AAJ82996
ID AAY82996 standard; peptide; 9 AA.

XX AC AAY82996;

XX DT 04-JUL-2000 (first entry)

XX Substituted hepatitis C virus core polypeptide antigenic fragment.

XX Hepatitis C virus; HCV; core polypeptide; antigen; epitope; agretope;
XX anchor residue; cytotoxic T lymphocyte; CTL; immune response; MHC;
XX Major histocompatibility complex; vaccine; treatment.

XX OS Synthetic.

XX OS Hepatitis C virus; (HCV).

XX FH Key Location/Qualifiers

XX FT Misc-difference 8 /label= Ala substituted for Leu

XX FT WO200011186-A1.

XX PN 02-MAR-2000.

XX PF 17-AUG-1999; 99WO-US018674.

XX PR 21-AUG-1998; 98US-0097446P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Berzofsky JA, Sarobe P, Pendleton CD, Feinstein SM, Arichi T;
XX PI Major ME;

XX DR WPI; 2000-246569/21.

XX PT Hepatitis C virus polypeptides is useful as a vaccine for treating

XX FT Hepatitis C virus infection and for activating cytotoxic T lymphocytes.

XX PS Claim 16; Page 71; 78pp; English.

XX CC Peptide fragments of the Hepatitis C virus (HCV) core polypeptide can be
XX used to elicit an immune response. A cytotoxic T-lymphocyte (CTL)
XX response is present in patients acutely and chronically infected by HCV.
XX CTL's recognise viral antigens as peptides presented by Class I molecules
XX of the major histocompatibility complex (MHC). These peptide antigens are
XX typically 8-10 amino acids long. These peptide antigens typically have a
XX sequence pattern or motif depending upon which particular MHC antigen
XX they are bound and presented by. The motifs are based on the presence in
XX precise positions in the peptide sequence of several amino acids
XX (agretopic residues) called anchor residues, responsible for interactions
XX between peptide and MHC molecule, as well as other secondary position
XX that may help to stabilise the interaction. Thus, single amino acid
XX changes within the peptide sequence can enhance the immune response.
XX Peptides derived from the HCV core polypeptide having substituted amino
XX acids within their sequence, specifically a hepatitis C virus core
XX polypeptide comprising an L to an A substitution at amino acid position
XX 139 enhance the immune response against HCV. They can therefore be used
XX as a vaccine or for treating HCV infection. This peptide is a fragment of
XX the substituted HCV core polypeptide and comprises the region of amino
XX acids within that polypeptide from position 132 to position 140 which
XX contains the amino acid substitution

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 47; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | |
DB 1 DLMGYIPAV 9

RESULT 2

AAJ82052
ID AAB82052 standard; peptide; 9 AA.

XX AC AAB82052;

XX DT 06-AUG-2003 (revised)

XX DT 22-JUN-2001 (first entry)

XX DE HCV antigen, core 132-140.

XX Antigen; immunostimulant; vaccine; pharmaceutical composition; antiviral;
XX viral infection.

XX OS Hepatitis C virus.

XX PN WO200124822-A2.

XX PD 12-APR-2001.

XX PF 02-OCT-2000; 2000WO-EP009657.

XX PR 01-OCT-1999; 99AT-00001680.

XX PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

XX PI Fleitmann J, Mattner F, Buschle M, Melling J;

XX DR WPI; 2001-290577/30.

XX PT New pharmaceutical composition comprising an antigen, an
XX immunostimulating substance and a polycationic polymer, useful in
XX manufacturing vaccines.

XX PS Claim 12; Page 16; 20pp; English.

XX CC The present invention relates to a pharmaceutical composition comprising
XX (a) an antigen; (b) an immunostimulating substance consisting of
XX neuroactive compounds, hormones, compounds having growth hormone activity
XX or their mixtures; and (c) a polycationic polymer. The present sequence
XX is an antigenic peptide derived from Hepatitis C virus, which was used in
XX the present invention. The composition is useful in manufacturing
XX vaccines. (Updated on 06-AUG-2003 to correct OS field.)

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 47; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | |
DB 1 DLMGYIPAV 9

RESULT 3

ADJ25899
ID ADL25899 standard; peptide; 15 AA.

XX AC ADL25899;

XX DT 17-JUN-2004 (first entry)

XX DE Synthetic peptide A86 derived from a conserved region of HCV.

KW HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;
 KW major histocompatibility complex; human leukocyte antigen.
 XX
 XX Synthetic.

XX WO2004024182-A2.

XX 25-MAR-2004.

XX 27-AUG-2003; 2003WO-EP009482.

XX 13-SEP-2002; 2002AT-00001376.

XX 27-FEB-2003; 2003WO-EP002005.

XX 11-JUL-2003; 2003EP-00450171.

XX (INTE-) INTERCELL AG.

XX Buschle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;

XX Zauner W, Zinke S, Kiriappos H;

XX WPI; 2004-269899/25.

XX Isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
 PT to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 PT molecule by separating the complex from the HCV-peptides which do not
 PT bind to the molecule.

XX Example 1; Page 30; 73pp; English.

XX The invention relates to a novel method for isolating Hepatitis C Virus
 CC (HCV) peptides (HPs). The method of the invention has virucide activity,
 CC and may be useful in producing a vaccine. The method is useful for
 CC isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
 CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 CC MHC/HLA molecule for preparing a vaccine against HCV infection. The T
 CC cells, a T cell clone or a T cell population or preparation is useful for
 CC identifying heteroclitic epitopes or for preparing a composition for
 CC treating HCV infection. The present sequence represents a synthetic
 CC peptide derived from a conserved region of HCV.

XX Sequence 15 AA;

Query Match 91.5%; Score 43; DB 8; Length 15;
 Best Local Similarity 88.9%; Pred. No. 0.095;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9

DB 7 DLMGYIPW 15

RESULT 4

ADL25904

ID ADL25904 standard; peptide; 15 AA.

XX ADL25904;

XX 17-JUN-2004 (first entry)

XX Synthetic peptide A91 derived from a conserved region of HCV.

XX HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;

XX major histocompatibility complex; human leukocyte antigen.

XX Synthetic.

XX WO2004024182-A2.

XX 25-MAR-2004.

XX 27-AUG-2003; 2003WO-EP009482.

XX 13-SEP-2002; 2002AT-00001376.

PR 27-FEB-2003; 2003WO-EP002005.

PR 11-JUL-2003; 2003EP-00450171.

XX (INTE-) INTERCELL AG.

XX Buschle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;

XX Zauner W, Zinke S, Kiriappos H;

XX WPI; 2004-269899/25.

XX Isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
 PT to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 PT molecule by separating the complex from the HCV-peptides which do not
 PT bind to the molecule.

XX Example 1; Page 30; 73pp; English.

XX The invention relates to a novel method for isolating Hepatitis C Virus
 CC (HCV) peptides (HPs). The method of the invention has virucide activity,
 CC and may be useful in producing a vaccine. The method is useful for
 CC isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
 CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 CC MHC/HLA molecule for preparing a vaccine against HCV infection. The T
 CC cells, a T cell clone or a T cell population or preparation is useful for
 CC identifying heteroclitic epitopes or for preparing a composition for
 CC treating HCV infection. The present sequence represents a synthetic
 CC peptide derived from a conserved region of HCV.

XX Sequence 15 AA;

Query Match 91.5%; Score 43; DB 8; Length 15;
 Best Local Similarity 88.9%; Pred. No. 0.095;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9

DB 2 DLMGYIPV 10

RESULT 5

ADL25905

ID ADL25905 standard; peptide; 15 AA.

XX ADL25905;

XX 17-JUN-2004 (first entry)

XX Synthetic peptide A92 derived from a conserved region of HCV.

XX HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;

XX major histocompatibility complex; human leukocyte antigen.

XX Synthetic.

XX WO2004024182-A2.

XX 25-MAR-2004.

XX 27-AUG-2003; 2003WO-EP009482.

XX 13-SEP-2002; 2002AT-00001376.

XX 27-FEB-2003; 2003WO-EP002005.

XX 11-JUL-2003; 2003EP-00450171.

XX (INTE-) INTERCELL AG.

XX Buschle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;

XX Zauner W, Zinke S, Kiriappos H;

XX WPI; 2004-269899/25.

XX Isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
 PT to a MHC/HLA molecule or a complex comprising the HCV-peptide and the

PT molecule by separating the complex from the HCV-peptides which do not
 PT bind to the molecule.
 XX
 PS Example 1; Page 30; 73pp; English.
 XX
 CC The invention relates to a novel method for isolating Hepatitis C Virus
 CC (HCV) peptides (HPs). The method of the invention has virucide activity,
 CC and may be useful in producing a vaccine. The method is useful for
 CC isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
 CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 CC MHC/HLA molecule for preparing a vaccine against HCV infection. The T
 CC cells, a T cell clone or a T cell population or preparation is useful for
 CC identifying heteroclitic epitopes or for preparing a composition for
 CC treating HCV infection. The present sequence represents a synthetic
 CC peptide derived from a conserved region of HCV.
 XX
 SQ Sequence 15 AA;
 Query Match 91.5%; Score 43; DB 8; Length 15;
 Best Local Similarity 88.9%; Pred. No. 0.095;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DLMGYIPAV 9
 Db |||||
 1 DLMGYIPV 9
 RESULT 6
 ADL25900
 ID ADL25900 standard; peptide; 15 AA.
 XX
 AC ADL25900;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Synthetic peptide A87 derived from a conserved region of HCV.
 XX
 KW HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;
 KW major histocompatibility complex; human leukocyte antigen.
 XX
 OS Synthetic.
 XX
 PN WO2004024182-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 27-AUG-2003; 2003WO-EP009482.
 XX
 PR 13-SEP-2002; 2002AT-00001376.
 PR 27-FEB-2003; 2003WO-EP002005.
 PR 11-JUL-2003; 2003EP-00450171.
 XX
 PA (INTE-) INTERCELL AG.
 XX
 PI Buschle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;
 PI Zauner W, Zinke S, Kirlappos H;
 XX
 PD WPI; 2004-269899/25.
 XX
 PF 27-AUG-2003; 2003WO-EP009482.
 XX
 PR 13-SEP-2002; 2002AT-00001376.
 PR 27-FEB-2003; 2003WO-EP002005.
 PR 11-JUL-2003; 2003EP-00450171.
 XX
 PA (INTE-) INTERCELL AG.
 XX
 PI Buschle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;
 PI Zauner W, Zinke S, Kirlappos H;
 XX
 PD WPI; 2004-269899/25.
 XX
 PF Isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
 PT to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 PT molecule by separating the complex from the HCV-peptides which do not
 PT bind to the molecule.
 XX
 PS Example 1; Page 30; 73pp; English.
 XX
 CC The invention relates to a novel method for isolating Hepatitis C Virus
 CC (HCV) peptides (HPs). The method of the invention has virucide activity,
 CC and may be useful in producing a vaccine. The method is useful for
 CC isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
 CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 CC MHC/HLA molecule for preparing a vaccine against HCV infection. The T
 CC cells, a T cell clone or a T cell population or preparation is useful for

CC identifying heteroclitic epitopes or for preparing a composition for
 CC treating HCV infection. The present sequence represents a synthetic
 CC peptide derived from a conserved region of HCV.
 XX
 SQ Sequence 15 AA;
 Query Match 91.5%; Score 43; DB 8; Length 15;
 Best Local Similarity 88.9%; Pred. No. 0.095;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DLMGYIPAV 9
 Db |||||
 6 DLMGYIPV 14
 RESULT 7
 ADL25901
 ID ADL25901 standard; peptide; 15 AA.
 XX
 AC ADL25901;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Synthetic peptide A88 derived from a conserved region of HCV.
 XX
 KW HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;
 KW major histocompatibility complex; human leukocyte antigen.
 XX
 OS Synthetic.
 XX
 PN WO2004024182-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 27-AUG-2003; 2003WO-EP009482.
 XX
 PR 13-SEP-2002; 2002AT-00001376.
 PR 27-FEB-2003; 2003WO-EP002005.
 PR 11-JUL-2003; 2003EP-00450171.
 XX
 PA (INTE-) INTERCELL AG.
 XX
 PI Buschle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;
 PI Zauner W, Zinke S, Kirlappos H;
 XX
 PD WPI; 2004-269899/25.
 XX
 PF Isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
 PT to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 PT molecule by separating the complex from the HCV-peptides which do not
 PT bind to the molecule.
 XX
 PS Example 1; Page 30; 73pp; English.
 XX
 CC The invention relates to a novel method for isolating Hepatitis C Virus
 CC (HCV) peptides (HPs). The method of the invention has virucide activity,
 CC and may be useful in producing a vaccine. The method is useful for
 CC isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
 CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 CC MHC/HLA molecule for preparing a vaccine against HCV infection. The T
 CC cells, a T cell clone or a T cell population or preparation is useful for
 CC identifying heteroclitic epitopes or for preparing a composition for
 CC treating HCV infection. The present sequence represents a synthetic
 CC peptide derived from a conserved region of HCV.
 XX
 SQ Sequence 15 AA;
 Query Match 91.5%; Score 43; DB 8; Length 15;
 Best Local Similarity 88.9%; Pred. No. 0.095;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DLMGYIPAV 9
 |||||

```

Db      5 DLGMYIPV 13

RESULT 8
ADL25903
ID      ADL25903 standard; peptide; 15 AA.
AC      ADL25903;
XX      17-JUN-2004 (first entry)
DT      Synthetic peptide A90 derived from a conserved region of HCV.
DE      HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;
XX      major histocompatibility complex; human leukocyte antigen.
KW      Synthetic.
XX      WO2004024182-A2.
XX      25-MAR-2004.
XX      27-AUG-2003; 2003WO-EP009482.
XX      13-SEP-2002; 2002AT-00001376.
XX      27-FEB-2003; 2003WO-EP002005.
XX      11-JUL-2003; 2003EP-00450171.
XX      (INTE-) INTERCELL AG.
XX      Buschle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;
XX      Zauner W, Zinke S, Kiriappos H;
XX      WPI; 2004-269899/25.
XX      Isolating Hepatitis C Virus peptides (Hps) which have a binding capacity
XX      to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
XX      molecule by separating the complex from the HCV-peptides which do not
XX      bind to the molecule.
XX      Example 1; Page 30; 73pp; English.
XX      The invention relates to a novel method for isolating Hepatitis C Virus
XX      (HCV) peptides (Hps). The method of the invention has virucide activity,
XX      and may be useful in producing a vaccine. The method is useful for
XX      isolating Hepatitis C Virus peptides (Hps) which have a binding capacity
XX      to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
XX      MHC/HLA molecule for preparing a vaccine against HCV infection. The T
XX      cells, a T cell clone or a T cell population or preparation is useful for
XX      identifying heteroclitic epitopes or for preparing a composition for
XX      treating HCV infection. The present sequence represents a synthetic
XX      peptide derived from a conserved region of HCV.
XX      Sequence 15 AA;
XX      Query Match      91.5%; Score 43; DB 8; Length 15;
XX      Best Local Similarity 88.9%; Pred. No. 0.095;
XX      Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1 DLGMYIPAV 9
Db      4 DLGMYIPV 12

RESULT 10
ADL26466
ID      ADL26466 standard; peptide; 36 AA.
XX      ADL26466;
XX      17-JUN-2004 (first entry)
DT      Synthetic peptide 1649 derived from a conserved region of HCV.
DE      HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;
XX      major histocompatibility complex; human leukocyte antigen.
XX      Synthetic.
XX      WO2004024182-A2.
XX      25-MAR-2004.
XX      27-AUG-2003; 2003WO-EP009482.
XX

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PR 13-SEP-2002; 2002AT-00001376.
PR 27-FEB-2003; 2003WO-EP002005.
PR 11-JUL-2003; 2003EP-00450171.
XX (INTE-) INTERCELL AG.
XX
XX Buechle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;
PI Zauner W, Zinke S, Kirlappos H;
XX WPI; 2004-269899/25.
XX
XX Isolating Hepatitis C Virus peptides (HVs) which have a binding capacity
PT to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
PT molecule by separating the complex from the HCV-peptides which do not
PT bind to the molecule.
XX
XX Example 1; Page 32; 73pp; English.
XX
XX The invention relates to a novel method for isolating Hepatitis C Virus
CC (HCV) peptides (HVs). The method of the invention has virucide activity,
CC and may be useful in producing a vaccine. The method is useful for
CC isolating Hepatitis C Virus peptides (HVs) which have a binding capacity
CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
CC MHC/HLA molecule for preparing a vaccine against HCV infection. The T
CC cells, a T cell clone or a T cell population or preparation is useful for
CC identifying heteroclitic epitopes or for preparing a composition for
CC treating HCV infection. The present sequence represents a synthetic
CC peptide derived from a conserved region of HCV.
XX
XX Sequence 36 AA;
SQ
XX
XX Query Match 91.5%; Score 43; DB 8; Length 36;
XX Best Local Similarity 88.9%; Pred. No. 0.25;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 DLMGYIPAV 9
XX | | | | |
XX 22 DLMGYIPVW 30
XX
XX RESULT 11
XX AAR73111
XX ID AAR73111 standard; peptide; 9 AA.
XX AC AAR73111;
XX
XX 25-MAR-2003 (revised)
XX 16-JUN-1995 (first entry)
XX
XX Antigen fragment 8 from HCV has binding affinity for HLA-2.1.
XX
XX antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV; HIV1;
XX plasma specific antigen; hepatitis B virus; Epstein Barr;
XX human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1;
XX melanoma antigen-1; core antigen; surface antigen;
XX pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic;
XX MHC class I molecule; major histocompatibility complex; HLA-A2.1; 9mer;
XX 10mer; anchor; human leukocyte antigen; PLP; 8mer; algorithm prediction;
XX MBP; CMV; cytomegalovirus; HSV; herpes simplex virus; influenza A; M1.
XX
XX Hepatitis C virus.
XX
XX WO9420127-A1.
XX
XX 15-SEP-1994.
XX
XX 04-MAR-1994; 94WO-US002353.
XX
XX 05-MAR-1993; 93US-00027146.
XX 04-JUN-1993; 93US-00073205.
XX 29-NOV-1993; 93US-00159184.
XX
XX (CYTE-) CYTEL CORP.
XX
XX Grey HM, Sette A, Sidney J, Kast W;
XX WPI; 1994-302678/37.
XX
XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for
PT treatment or prophylaxis of cancer, virus infection or autoimmune
PT diseases.
XX
XX Disclosure; Page 90; 138pp; English.
XX
XX AAR73058-121 are potential peptide binders of HLA-A2.1 motif. Using
CC motifs disclosed in the invention, these peptides were screened for
CC further motifs. Only peptides with binding affinity of at least 1%
CC (binding affinity is expressed as an IC50 value) as compared to the
CC standard peptide (AAR71293) in assays. This peptide from hepatitis C
CC virus has a binding value of 0.0550. The peptides of the invention can
CC induce cytotoxic T lymphocytes which can react with target cells. They
CC can be used for the treatment or prophylaxis of cancer, eg, prostate
CC cancer or lymphoma, etc. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 9 AA;
SQ
XX
XX Query Match 89.4%; Score 42; DB 2; Length 9;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+06;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 DLMGYIPAV 9
XX | | | | |
XX 1 DLMGYIPLV 9
XX
XX RESULT 12
XX AAR59125
XX ID AAR59125 standard; peptide; 9 AA.
XX AC AAR59125;
XX
XX 16-OCT-2003 (revised)
XX 25-MAR-2003 (revised)
XX 02-MAY-1995 (first entry)
XX
XX Peptide fragment (1.0816) of HCV binds HLA-A2.1.
XX
XX antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV; HIV1;
XX core antigen; surface antigen; pharmaceutical composition; in vivo;
XX ex vivo; therapeutic; diagnostic; MHC class I molecule;
XX major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;
XX human leukocyte antigen.
XX
XX Hepatitis C virus; strain.
XX
XX WO9420127-A1.
XX
XX 15-SEP-1994.
XX
XX 04-MAR-1994; 94WO-US002353.
XX
XX 05-MAR-1993; 93US-00027146.
XX 04-JUN-1993; 93US-00073205.
XX 29-NOV-1993; 93US-00159184.
XX
XX (CYTE-) CYTEL CORP.
XX
XX Grey HM, Sette A, Sidney J, Kast W;
XX WPI; 1994-302678/37.
XX
XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for
PT treatment or prophylaxis of cancer, virus infection or autoimmune
PT diseases.
XX
XX Example 5; Page 100; 138pp; English.
XX
XX

```


Best Local Similarity 88.9%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
| | | | | | |
Db 1 DLMGYIPLV 9

RESULT 18

AAV10219

ID AAY10219 standard; peptide; 9 AA.

XX AC AAY10219;

XX DT 12-MAY-1999 (first entry)

XX DE T cell epitope/MHC ligand SEQ ID NO:149.

XX KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;

XX KW immunisation; tumour; infectious disease; immunotherapy; cancer;

XX KW malignant melanoma; viral disease; hepatitis; AIDS.

XX OS Synthetic.

XX OS Hepatitis C virus.

XX PN WO9902183-A2.

XX PD 21-JAN-1999.

XX PF 10-JUL-1998; 98WO-US014289.

XX PR 10-JUL-1997; 97CA-02209815.

XX PR 10-DEC-1997; 97US-00988320.

XX PA (CTL1-) CTL IMMUNOTHERAPIES CORP.

XX PI Kuendig TM, Simard JJJ;

XX DR WPI; 1999-120514/10.

XX PT Inducing a cytotoxic T lymphocyte response - by maintaining a level of

XX PT antigen in the lymphatic system of a mammal so as to provide a sustained

XX PT CTL response, used to treat, e.g. AIDS.

XX PS Disclosure; Page 29; 199pp; English.

XX CC The present invention describes a method of inducing and/or sustaining an

XX CC immunological cytotoxic T lymphocyte (CTL) response in a mammal. The

XX CC method comprises: (a) delivering an antigen to the mammal at a level to

XX CC induce an immunological CTL response in the mammal; and (b) maintaining

XX CC the level of the antigen in the mammal's lymphatic system to maintain the

XX CC immunologic CTL response. The method can be used for the delivery of e.g.

XX CC a differentiation antigen, an oncogene antigen, a mutated tumour-suppressor gene

XX CC embryonic antigen, or a viral antigen. They can be used for the treatment of

XX CC disease such as cancer, e.g. malignant melanoma or infectious disease.

XX CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery

XX CC to the lymphatic system provides for potent CTL stimulation that takes

XX CC place in the milieu of the lymphoid organ, and it sustains stimulation

XX CC that is necessary to keep CTL active, cytotoxic and recirculating through

XX CC the body. AAY10071 to AAY10639 represent examples of peptide antigens

XX CC given in the present invention

XX SQ Sequence 9 AA;

Query Match 89.4%; Score 42; DB 2; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.8e+06;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9

| | | | | | |

Db 1 DLMGYIPLV 9

XX AC AAY73106

XX XX AAY73106 standard; peptide; 9 AA.

XX AC AAY73106;

XX XX

RESULT 19

AAV10441

ID AAY10441 standard; peptide; 9 AA.

XX AC AAY10441;

XX DT 12-MAY-1999 (first entry)

XX DE HLA Class I motif peptide SEQ ID NO:371.

XX KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;

XX KW immunisation; tumour; infectious disease; immunotherapy; cancer;

XX KW malignant melanoma; viral disease; hepatitis; AIDS.

XX OS Synthetic.

XX OS Human papillomavirus.

XX PN WO9902183-A2.

XX PD 21-JAN-1999.

XX PF 10-JUL-1998; 98WO-US014289.

XX PR 10-JUL-1997; 97CA-02209815.

XX PR 10-DEC-1997; 97US-00988320.

XX PA (CTL1-) CTL IMMUNOTHERAPIES CORP.

XX PI Kuendig TM, Simard JJJ;

XX DR WPI; 1999-120514/10.

XX PT Inducing a cytotoxic T lymphocyte response - by maintaining a level of

XX PT antigen in the lymphatic system of a mammal so as to provide a sustained

XX PT CTL response, used to treat, e.g. AIDS.

XX PS Disclosure; Page 40; 199pp; English.

XX CC The present invention describes a method of inducing and/or sustaining an

XX CC immunological cytotoxic T lymphocyte (CTL) response in a mammal. The

XX CC method comprises: (a) delivering an antigen to the mammal at a level to

XX CC induce an immunological CTL response in the mammal; and (b) maintaining

XX CC the level of the antigen in the mammal's lymphatic system to maintain the

XX CC immunologic CTL response. The method can be used for the delivery of e.g.

XX CC a differentiation antigen, an oncogene antigen, a mutated tumour-suppressor gene

XX CC embryonic antigen, or a viral antigen. They can be used for the treatment of

XX CC disease such as cancer, e.g. malignant melanoma or infectious disease.

XX CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery

XX CC to the lymphatic system provides for potent CTL stimulation that takes

XX CC place in the milieu of the lymphoid organ, and it sustains stimulation

XX CC that is necessary to keep CTL active, cytotoxic and recirculating through

XX CC the body. AAY10071 to AAY10639 represent examples of peptide antigens

XX CC given in the present invention

XX SQ Sequence 9 AA;

Query Match 89.4%; Score 42; DB 2; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.8e+06;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9

| | | | | | |

Db 1 DLMGYIPLV 9

XX AC AAY73106

XX XX AAY73106 standard; peptide; 9 AA.

XX AC AAY73106;

XX XX

```

DT 06-AUG-2003 (revised)
DE 28-FEB-2000 (first entry)
DE Hepatitis C virus (HCV)-derived MHC class I (CTL) epitope, #264.
XX
XX Chimeric; pan DR epitope; expression vector; promoter;
KW major histocompatibility complex; MHC; targeting; peptide; epitope;
KW antigen; presentation; class I; cytosolic pathway; endoplasmic reticulum;
KW class II; extracellular antigen; endocytic pathway; helper T lymphocyte;
KW HTL; universal epitope; cytotoxic T lymphocyte; CTL; immune response;
KW immunogenicity; assay; vaccine; immunity; infection; pathogen; virus;
KW HIV; HBV; HCV; hepatitis B; hepatitis C; bacterium; protozoan;
KW tumour cell; autoimmune disease; activation; antiviral; antimalarial;
KW immunoprotective.
XX
XX Synthetic.
OS
OS Hepatitis C virus.
XX
XX WO9958658-A2.
XX
XX 18-NOV-1999.
XX
XX 13-MAY-1999; 99WO-US010646.
XX
XX 13-MAY-1998; 98US-00078904.
XX
XX 15-MAY-1998; 98US-0085751P.
XX
XX (EPIM-) EPIMMUNE INC.
XX
XX Fikes JD, Hermanson GG, Sette A, Ishioka GY, Livingston B;
PI Chesnut RW;
PI
XX
XX WPI; 2000-039103/03.
XX
XX Expression vectors encoding major histocompatibility targeting sequence,
PT used as, e.g. tumor vaccines.
XX
XX Claim 11; Page 68; 130pp; English.
XX
XX Sequences AAY73103-Y73145 represent hepatitis C virus (HCV)-derived MHC
CC class I (CTL) epitopes which are claimed for use in the present
CC invention. The invention relates to a novel expression vector comprising
CC a promoter operably linked to a fusion gene encoding a major
CC histocompatibility complex (MHC) targeting sequence, and two or more
CC heterologous peptide epitopes. The MHC targeting sequence may be a class
CC I targeting sequence, which directs an MHC class I epitope to a
CC cytosolic pathway or to the endoplasmic reticulum, or an MHC class II
CC targeting sequence, which directs extracellular antigens to enter the
CC endocytic pathway to be processed into antigen peptides for presentation
CC on MHC class II molecules. The heterologous epitopes may comprise either
CC helper T lymphocyte (HTL) epitopes, or a cytotoxic T lymphocyte (CTL)
CC epitope and a universal HTL epitope such as a pan DR epitope (PADRE). The
CC vectors are useful for stimulating an immune response in vivo, as well as
CC for use in assaying the human immunogenicity of a human T cell peptide
CC epitope in vivo in a non-human mammal. They provide a nucleic acid
CC vaccine for enhancing immunity against infectious pathogens, such as
CC viruses (e.g., HIV, hepatitis B (HBV) and hepatitis C (HCV)), bacteria,
CC protozoa (e.g., Plasmodium falciparum, the cause of malaria) and also
CC tumour cells and autoimmune diseases. Universal MHC class II epitopes are
CC advantageously combined with other MHC class I and class II epitopes to
CC increase the number of cells that are activated in response to a given
CC antigen and provide a broader population coverage of MHC-reactive
CC alleles. (Updated on 06-AUG-2003 to correct OS field.)
XX
XX Sequence 9 AA;
SQ
Query Match 89.4%; Score 42; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DLMGYIPAV 9
DB 1 DLMGYIPLV 9
RESULT 22

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RESULT 21
AAY82998
ID AAY82998 standard; peptide; 9 AA.
XX
XX AAY82998;
AC
XX 12-SEP-2003 (revised)
DT 04-JUL-2000 (first entry)
XX
XX Hepatitis C virus core polypeptide antigenic fragment.
DE
XX Hepatitis C virus; HCV; core polypeptide; antigen; epitope; agretope;
KW anchor residue; cytotoxic T lymphocyte; CTL; immune response; MHC;
KW Major histocompatibility complex; vaccine; treatment.
XX
XX Hepatitis C virus; (HCV).
OS
XX WO200011186-A1.
XX
XX 02-MAR-2000.
XX
XX 17-AUG-1999; 99WO-US018674.
XX
XX 21-AUG-1998; 98US-0097446P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Berzofsky JA, Sarobe P, Pendleton CD, Feinstein SM, Arichi T;
PI Major ME;
XX
XX WPI; 2000-246569/21.
XX
XX Hepatitis C virus polypeptides is useful as a vaccine for treating
PT Hepatitis C virus infection and for activating cytotoxic T lymphocytes.
XX
XX Claim 33; Page 72; 78pp; English.
XX
XX Peptide fragments of the Hepatitis C virus (HCV) core polypeptide can be
CC used to elicit an immune response. A cytotoxic T-lymphocyte (CTL)
CC response is present in patients acutely and chronically infected by HCV.
CC CTL's recognise viral antigens as peptides presented by Class I molecules
CC of the major histocompatibility complex (MHC). These peptide antigens are
CC typically 8-10 amino acids long. These peptide antigens typically have a
CC sequence pattern or motif depending upon which particular MHC antigen
CC they are bound and presented by. The motifs are based on the presence in
CC precise positions in the peptide sequence of several amino acids
CC (agretopic residues) called anchor residues, responsible for interactions
CC between peptide and MHC molecule, as well as other secondary position
CC that may help to stabilise the interaction. Thus, single amino acid
CC changes within the peptide sequence can enhance the immune response.
CC Peptides derived from the HCV core polypeptide having substituted amino
CC acids within their sequence, specifically a hepatitis C virus core
CC polypeptide comprising an L to an A substitution at amino acid position
CC 139 enhance the immune response against HCV. They can therefore be used
CC as a vaccine or for treating HCV infection. This peptide is derived from
CC the wild type HCV core polypeptide and comprises the region of amino
CC acids within that polypeptide from position 132 to position 140. (Updated
CC on 12-SEP-2003 to standardise OS field)
XX
XX Sequence 9 AA;
SQ
Query Match 89.4%; Score 42; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DLMGYIPAV 9
DB 1 DLMGYIPLV 9
RESULT 22

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```
AAJ03866
ID AAJ03866 standard; peptide; 9 AA.
AC AAJ03866;
XX
DT 02-JUL-2001 (first entry)
XX
DE Hepatitis C virus epitope #3857.
XX
KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX
OS Hepatitis C virus.
XX
PN WO200121189-A1.
XX
PD 29-MAR-2001.
XX
PF 19-JUL-2000; 2000WO-US019774.
XX
PR 19-JUL-1999; 99US-00357737.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-308046/32.
XX
PT A new composition useful as a vaccines against hepatitis C virus.
XX
PS Disclosure; Page 144; 214pp; English.
XX
CC The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention
XX
SQ Sequence 9 AA;

Query Match 89.4%; Score 42; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 1 DLMGYIPLV 9

RESULT 24
AAJ03964
ID AAJ03964 standard; peptide; 9 AA.
XX
AC AAJ03964;
XX
DT 02-JUL-2001 (first entry)
XX
DE Hepatitis C virus epitope #3955.
XX
KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW antiviral.
XX
OS Hepatitis C virus.
XX
PN WO200121189-A1.
XX
PD 29-MAR-2001.
XX
PF 19-JUL-2000; 2000WO-US019774.
XX
PR 19-JUL-1999; 99US-00357737.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-308046/32.
XX
PT A new composition useful as a vaccines against hepatitis C virus.
XX
PS Example 3; Page 196; 214pp; English.
XX
CC The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention
XX
SQ Sequence 9 AA;

Query Match 89.4%; Score 42; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 1 DLMGYIPLV 9

RESULT 23
AAJ01746
ID AAJ01746 standard; peptide; 9 AA.
XX
AC AAJ01746;
XX
DT 02-JUL-2001 (first entry)
XX
DE Hepatitis C virus epitope #1737.
XX
KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW antiviral.
XX
OS Hepatitis C virus.
XX
PN WO200121189-A1.
XX
PD 29-MAR-2001.
XX
PF 19-JUL-2000; 2000WO-US019774.
XX
PR 19-JUL-1999; 99US-00357737.
XX
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Qy      1 DLMGYIPAV 9
Db      1 DLMGYIPLV 9

RESULT 25
AAJ00011
ID AAJ00011 standard; peptide; 9 AA.
XX AC
XX AAJ00011;
DT 02-JUL-2001 (first entry)
XX DE Hepatitis C virus epitope #2.
XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX OS Hepatitis C virus.
XX PN WO200121189-A1.
XX PD 29-MAR-2001.
XX PF 19-JUL-2000; 2000WO-US019774.
XX PR 19-JUL-1999; 99US-00357737.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Cellis E, Kubo RT, Grey HM;
XX DR WPI; 2001-308046/32.
XX SQ Sequence 9 AA;

Query Match      89.4%; Score 42; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
Db      1 DLMGYIPLV 9

RESULT 27
AAJ03787
ID AAJ03787 standard; peptide; 9 AA.
XX AC
XX AAJ03787;
DT 02-JUL-2001 (first entry)
XX DE Hepatitis C virus epitope #3778.
XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX OS Hepatitis C virus.
XX PN WO200121189-A1.
XX PD 29-MAR-2001.
XX PF 19-JUL-2000; 2000WO-US019774.
XX PR 19-JUL-1999; 99US-00357737.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Cellis E, Kubo RT, Grey HM;
XX DR WPI; 2001-308046/32.
XX SQ A new composition useful as a vaccines against hepatitis C virus.
Disclosure; Page 106; 214pp; English.
The present invention describes a composition comprising a prepared
hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
These are derived from HCV HLA-binding motifs. They are useful in
vaccines for the prevention and treatment of HCV infection in humans. The
present sequence is an epitope used in the disclosure of the invention
Sequence 9 AA;

Query Match      89.4%; Score 42; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
Db      1 DLMGYIPLV 9

RESULT 26
AAJ00229
ID AAJ00229 standard; peptide; 9 AA.
XX AC
XX AAJ00229;
DT 02-JUL-2001 (first entry)
XX DE Hepatitis C virus epitope #220.
XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX OS Hepatitis C virus.
XX PN WO200121189-A1.

```

CC present sequence is an epitope used in the disclosure of the invention
 XX Sequence 9 AA;
 SQ

Query Match 89.4%; Score 42; DB 4; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
 ||||| |
 Db 1 DLMGYIPLV 9

RESULT 28
 AAJ04086
 ID AAJ04086 standard; peptide; 9 AA.
 XX
 AC AAJ04086;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #4077.
 XX
 DE Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX
 XX Hepatitis C virus.
 OS
 XX WO200121189-A1.
 PN
 XX 29-MAR-2001.
 PD
 XX 19-JUL-2000; 2000WO-US019774.
 PF
 XX 19-JUL-1999; 99US-003577737.
 PR
 XX (EPIW-) EPIMUNE INC.
 PA
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 FI
 XX WPI; 2001-308046/32.
 DR
 XX A new composition useful as a vaccines against hepatitis C virus.
 PT
 XX Example 7; Page 203; 21app; English.
 PS
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention
 XX
 SQ Sequence 9 AA;

Query Match 89.4%; Score 42; DB 4; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
 ||||| |
 Db 1 DLMGYIPLV 9

RESULT 29
 ABG79901
 ID ABG79901 standard; peptide; 9 AA.
 XX
 AC ABG79901;
 XX
 DT 15-NOV-2002 (first entry)
 DE
 XX MHC class I molecule, viral epitope #149.

XX Major histocompatibility complex; MHC; MHC class I molecule; virus;
 KW epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;
 KW antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;
 KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;
 KW acquired immune deficiency syndrome; AIDS.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200262368-A2.
 XX
 PD 15-AUG-2002.
 XX
 PF 22-JAN-2002; 2002WO-US002033.
 XX
 PR 02-FEB-2001; 2001US-00776232.
 XX
 PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
 XX
 PI Kundig TM, Simard JVL;
 XX
 DR WPI; 2002-657506/70.
 XX
 DR Inducing or sustaining immunological cytotoxic T lymphocyte response in a
 PT mammal, useful for treating a mammal with malignant tumor or infectious
 PT disease, by directly administering an antigen to the lymphatic system of
 PT the mammal.
 XX
 PS Disclosure; Page 22; 73pp; English.
 XX
 CC The invention relates to a method of inducing and/or sustaining an
 CC immunological cytotoxic T lymphocyte (CTL) response in a mammal
 CC comprising administering directly to the lymphatic system of the mammal:
 CC (a) an antigen in the form of a polypeptide; (b) a vector comprising a
 CC nucleic acid encoding the antigen; or (c) a non-peptide antigen. The
 CC method is useful for inducing and/or sustaining CTL response in a mammal.
 CC This is particularly useful for treating a mammal having a malignant
 CC tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious
 CC disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS),
 CC malaria, measles or tuberculosis), or in an animal having a
 CC predisposition to these diseases. The mammal may be dogs, cats, mice,
 CC cattle, sheep, pigs, goats, rabbits, or preferably humans. ABG79753-
 CC ABG80319 represent viral epitopes on major histocompatibility complex
 CC (MHC) class I molecules, used in the method of the invention
 XX
 SQ Sequence 9 AA;

Query Match 89.4%; Score 42; DB 5; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
 ||||| |
 Db 1 DLMGYIPLV 9

RESULT 30
 ABG80124
 ID ABG80124 standard; peptide; 9 AA.
 XX
 AC ABG80124;
 XX
 DT 29-AUG-2003 (revised)
 DT 15-NOV-2002 (first entry)
 XX
 DE MHC class I molecule, viral epitope #372.
 XX
 KW Major histocompatibility complex; MHC; MHC class I molecule; virus;
 KW epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;
 KW antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;
 KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;
 KW acquired immune deficiency syndrome; AIDS.
 XX

CC The invention relates to a method of designing multi-epitope constructs
 CC comprising major histocompatibility complex (MHC) class I and II (CTL)
 CC epitope nucleic acids (CEN), involves sorting CEN, introducing flanking
 CC amino acid residue selected from specified amino acid residues given in
 CC specification at C+1 position of CEN, introducing amino acid spacer
 CC residues between two CEN, and selecting the constructs having less
 CC junctional epitopes. The method is useful for designing a multi-epitope
 CC construct having multiple epitope nucleic acid. The method avoids or
 CC minimises the occurrence of junctional epitopes and maximises the
 CC immunogenicity and/or antigenicity of multi-epitope vaccines. The present
 CC sequence represents the amino acid sequence of an epitope present in a
 CC multi-epitope construct.

XX Sequence 9 AA;

Query Match 89.4%; Score 42; DB 7; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 DB 1 DLMGYIPLV 9
 |||||

RESULT 33
 ADE97587
 ID ADE97587 standard; peptide; 9 AA.

XX AC ADE97587;

XX DT 12-FEB-2004 (first entry)

XX DE Immunogenic HLA-A2.1 binding peptide #69.

XX cytostatic; anti-inflammatory; hepatotropic; virucide; anti-HIV;
 XX nephrotropic; neuroprotective; antiarthritic; antirheumatic;
 XX immunosuppressive; dermatological; muscular; nephrotropic; thyromimetic;
 XX haemostatic; antithyroid; antianemic; anabolic; hypertensive;
 XX immunogenic peptide composition; immune response; prostate cancer;
 XX hepatitis B; hepatitis C; AIDS; renal carcinoma; cervical carcinoma;
 XX lymphoma; cytomegalovirus; CMV; condyloma acuminatum;
 XX autoimmune associated disorder; multiple sclerosis; rheumatoid arthritis;
 XX Sjogren syndrome; scleroderma; polymyositis; dermatomyositis;
 XX systemic lupus erythematosus; juvenile rheumatoid arthritis;
 XX ankylosing spondylitis; myasthenia gravis; MG; bullous pemphigoid;
 XX pemphigus; glomerulonephritis; Goodpasture's syndrome;
 XX autoimmune haemolytic anaemia; Hashimoto's disease; pernicious anaemia;
 XX idiopathic thrombocytopenic purpura; Grave's disease; Addison's disease;
 XX human leukocyte antigen A2.1; HLA A2.1;
 XX immunogenic HLA-A2.1 binding peptide.

XX OS Synthetic.

XX PN US2003185822-A1.

XX PD 02-OCT-2003.

XX PF 03-APR-2002; 2002US-00116557.

XX PR 05-MAR-1993; 93US-00027146.

XX PR 04-JUN-1993; 93US-00073205.

XX PR 29-NOV-1993; 93US-00159184.

XX PR 02-DEC-1994; 94US-00349177.

XX PA (GREY/) GREY H M.

XX PA (SETT/) SETTE A.

XX PA (SIDN/) SIDNEY J.

XX PI Grey HM, Sette A, Sidney J;

XX DR WPI; 2004-041186/04.

XX PT Immunogenic peptide composition for preventing, treating or diagnosing

PT pathological states, e.g. prostate cancer, hepatitis B and C, Acquired
 PT Immunodeficiency Syndrome, and renal carcinoma, includes conserved
 PT residues at specified positions.

XX Example 11; Page 23; 38pp; English.

XX The invention describes an immunogenic peptide composition comprising 9
 CC residues including a first conserved residue at a second position from N-
 CC terminus, and a second conserved residue at C-terminal position. The
 CC inventive peptide composition is used to elicit an immune response
 CC against a desired antigen for preventing, treating or diagnosing
 CC pathological states, e.g. prostate cancer, hepatitis B, hepatitis C,
 CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, cytomegalovirus
 CC (CMV), and condyloma acuminatum. It is also used to treat autoimmune
 CC associated disorders, e.g. multiple sclerosis, rheumatoid arthritis,
 CC Sjogren syndrome, scleroderma, polymyositis, dermatomyositis, systemic
 CC lupus erythematosus, juvenile rheumatoid arthritis, ankylosing
 CC spondylitis, myasthenia gravis (MG), bullous pemphigoid, pemphigus,
 CC glomerulonephritis, Goodpasture's syndrome, autoimmune hemolytic anemia,
 CC Hashimoto's disease, pernicious anaemia, idiopathic thrombocytopenic
 CC purpura, Grave's disease, and Addison's disease. The invention defines
 CC positions within a motif enabling the selection of the peptides, which
 CC will bind efficiently to human leukocyte antigen (HLA) A2.1. This is the
 CC amino acid sequence of an immunogenic HLA-A2.1 binding peptide.

XX Sequence 9 AA;

Query Match 89.4%; Score 42; DB 8; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 DB 1 DLMGYIPLV 9
 |||||

RESULT 34

ADJ79563

ID ADJ79563 standard; peptide; 9 AA.

XX AC ADJ79563;

XX DT 06-MAY-2004 (first entry)

XX CTL epitope for the HCV CORE protein HLA type A2 SeqID 72.

DE bacterial host system; polypeptide; vaccine; cytotoxic T-cell lymphocyte;
 XX Hepatitis C virus; HCV; infectious mononucleosis;
 KW nasopharyngeal carcinoma; virucidal; cytostatic; hepatotropic;
 KW antiinflammatory; anti-HIV; CTL; epitope; NS4.

XX OS Hepatitis C virus.

XX PN WO2004007556-A1.

XX PD 22-JAN-2004.

XX PF 14-JUL-2003; 2003WO-AU000910.

XX PR 12-JUL-2002; 2002AU-00950183.

XX PA (CSLC-) CSL LTD.

XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.

XX PI Webb EA, Schoofs P;

XX DR WPI; 2004-122896/12.

XX Designing a candidate polypeptide for expression in a host, useful for
 PT preventing or treating e.g. HIV, comprises identifying hydrophobic
 PT peptide sequences in the polypeptide and arranging or re-locating the
 PT peptide sequences.

PS Example 4; SEQ ID NO 72; 98pp; English.

XX This invention relates to a novel method for designing heterologous

CC polypeptides comprising a proportion of hydrophobic amino acids that

CC increases the probability of the protein being efficiently expressed in a

CC bacterial host system. Specifically, it refers to arranging or re-

CC locating a hydrophobic peptide sequence within the protein of interest in

CC order to generate a candidate protein with reduced amplitude in

CC hydrophobicity and/or length of any hydrophobic region. The present

CC invention describes using these polypeptides for use in a polypeptide

CC vaccine that is capable of eliciting a cytotoxic T-cell lymphocyte (CTL)

CC immune response. As such, compositions can be used for the prevention or

CC treatment of diseases associated with the Epstein-Barr virus (EBV) such

CC as infectious mononucleosis or nasopharyngeal carcinoma, as well as

CC hepatitis C virus, cytomegalovirus or HIV. Accordingly, they exhibit

CC antiviral, cytostatic, hepatotropic, antiinflammatory and anti-HIV

CC activities. This peptide sequence is a CTL epitope that can be included

CC in the HCV vaccine of the invention.

XX

SQ Sequence 9 AA;

Query Match 89.4%; Score 42; DB 8; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.8e+06; Mismatches 1; Indels 0; Gaps 0;

Matches 8; Conservative 0;

Qy 1 DLMGYIPAV 9

Db 1 DLMGYIPLV 9

|||||

RESULT 35

ID ADK69063 standard; peptide; 9 AA.

XX ADK69063;

DT 06-MAY-2004 (first entry)

XX

DE Epitope liberation-related peptide SeqID426.

XX

KW epitope liberation; substrate; proteasome; cytostatic; antibacterial;

KW protozoicide; fungicide; T-cell activator; vaccine; housekeeping epitope;

KW cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;

KW virus; bacterium; protozoan; fungus; housekeeping proteasome system.

XX

OS Human herpesvirus 5.

XX

PN US2003228634-A1.

XX

PD 11-DEC-2003.

XX

PF 07-NOV-2002; 2002US-00292413.

XX

PR 07-NOV-2001; 2001US-0336968P.

XX

PA (SIMA/) SIMARD J J L.

PA (DIAM/) DIAMOND D C.

PA (QIUZ/) QIU Z.

PA (LEIX/) LEI X.

XX

PI Simard J J L, Diamond DC, Qiu Z, Lei X;

XX

DR WPI; 2004-167209/16.

XX

PT Identifying polypeptide suitable for epitope e.g., housekeeping epitope,

PT liberation by contacting substrate polypeptide comprising epitope of

PT interest, with proteasome, and assaying for liberation of epitope.

XX

PS Disclosure; SEQ ID NO 426; 67pp; English.

XX

CC This invention relates to a novel method of identifying a polypeptide

CC suitable for epitope liberation, including the steps of identifying an

CC epitope of interest, providing substrate polypeptide sequence including

CC

the epitope, wherein the substrate permits processing by a proteasome;

contacting the substrate with a composition including the proteasome;

under conditions that support processing of the substrate by proteasome;

and assaying for liberation of epitope. The invention may be useful for

the development of compounds with a cytostatic, antibacterial,

protozoicide or fungicide activity acting as T-cell activators. In

addition, the invention may allow development of a vaccine. The invention

is useful for identifying a polypeptide suitable for epitope liberation,

where the epitope is a housekeeping epitope. The compositions comprising

the identified housekeeping epitopes are useful in vitro in vaccine

development or in the generation or expansion of cytotoxic T lymphocyte

(CTL) to be used in adoptive immunotherapy. The invention is also useful

for activating T-cells against neoplastic cells, and cells infected with

virus, bacterium, protozoan or fungus. CTL epitopes are identified based

on the knowledge that such epitopes are, in fact, produced by the

housekeeping proteasome system. Once identified, these epitopes, embodied

as peptides, can be used to successfully immunise or induce therapeutic

CTL responses against housekeeping proteasome expressing target cells in

the host. The present sequence is that of a peptide which is related to

the method of the invention.

XX

SQ Sequence 9 AA;

Query Match 89.4%; Score 42; DB 8; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.8e+06; Mismatches 1; Indels 0; Gaps 0;

Matches 8; Conservative 0;

Qy 1 DLMGYIPAV 9

Db 1 DLMGYIPLV 9

|||||

RESULT 36

ID ADK68837 standard; peptide; 9 AA.

XX ADK68837;

DT 06-MAY-2004 (first entry)

XX

DE Epitope liberation-related peptide SeqID200.

XX

KW epitope liberation; substrate; proteasome; cytostatic; antibacterial;

KW protozoicide; fungicide; T-cell activator; vaccine; housekeeping epitope;

KW cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;

KW virus; bacterium; protozoan; fungus; housekeeping proteasome system.

XX

OS Hepatitis C virus.

XX

PN US2003228634-A1.

XX

PD 11-DEC-2003.

XX

PF 07-NOV-2002; 2002US-00292413.

XX

PR 07-NOV-2001; 2001US-0336968P.

XX

PA (SIMA/) SIMARD J J L.

PA (DIAM/) DIAMOND D C.

PA (QIUZ/) QIU Z.

PA (LEIX/) LEI X.

XX

PI Simard J J L, Diamond DC, Qiu Z, Lei X;

XX

DR WPI; 2004-167209/16.

XX

PT Identifying polypeptide suitable for epitope e.g., housekeeping epitope,

PT liberation by contacting substrate polypeptide comprising epitope of

PT interest, with proteasome, and assaying for liberation of epitope.

XX

PS Disclosure; SEQ ID NO 200; 67pp; English.

XX

CC This invention relates to a novel method of identifying a polypeptide

CC suitable for epitope liberation, including the steps of identifying an
 CC epitope of interest; providing substrate polypeptide sequence including
 CC the epitope, wherein the substrate permits processing by a proteasome;
 CC contacting the substrate with a composition including the proteasome;
 CC under conditions that support processing of the substrate by proteasome;
 CC and assaying for liberation of epitope. The invention may be useful for
 CC the development of compounds with a cytostatic, antibacterial,
 CC prozoacide or fungicide activity acting as T-cell activators. In
 CC addition, the invention may allow development of a vaccine. The invention
 CC is useful for identifying a polypeptide suitable for epitope liberation,
 CC where the epitope is a housekeeping epitope. The compositions comprising
 CC the identified housekeeping epitopes are useful in vitro in vaccine
 CC development or in the generation or expansion of cytotoxic T lymphocyte
 CC (CTL) to be used in adoptive immunotherapy. The invention is also useful
 CC for activating T-cells against neoplastic cells, and cells infected with
 CC virus, bacterium, protozoan or fungus. CTL epitopes are identified based
 CC on the knowledge that such epitopes are, in fact, produced by the
 CC housekeeping proteasome system. Once identified, these epitopes, embodied
 CC as peptides, can be used to successfully immunise or induce therapeutic
 CC CTL responses against housekeeping proteasome expressing target cells in
 CC the host. The present sequence is that of a peptide which is related to
 CC the method of the invention.

XX Sequence 9 AA;

Query Match 89.4%; Score 42; DB 8; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 Db 1 DLMGYIPLV 9

RESULT 37

ID ADJ84718 standard; peptide; 9 AA.

XX ADJ84718;

DT 06-MAY-2004 (first entry)

XX Hepatitis C virus core protein CTL epitope SEQ ID NO:176.

XX lipopeptide; lipid moiety; T helper cell epitope; Th epitope;
 KW cytotoxic T cell epitope; CTL epitope; immune response; immunisation;
 KW influenza; hepatitis C virus; Listeria monocytogenes; vaccine; cancer;
 KW cytostatic; virucide.

OS Hepatitis C virus.
 OS Synthetic.

PN WO2004014957-A1.

XX 19-FEB-2004.

XX 12-AUG-2003; 2003WO-AU001019.

XX 12-AUG-2002; 2002US-0403328P.

XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.

XX Jackson D, Zeng W;

XX WPI; 2004-238736/22.

XX New lipopeptide comprising a polypeptide comprising an amino acid
 PT sequence of a T helper cell and cytotoxic T cell epitope, useful for
 PT preparing a composition for treating or preventing cancer, or hepatitis C
 PT virus or influenza virus.

PS Claim 22; SEQ ID NO 176; 166pp; English.

CC The present invention describes a lipopeptide comprising a polypeptide
 CC conjugated to one or more lipid moieties, where the polypeptide comprises
 CC an amino acid sequence that comprises: (a) the amino acid sequence of a T
 CC helper cell (Th) epitope and the amino acid sequence of a cytotoxic T
 CC cell (CTL) epitope, where the amino acid sequences are different; and (b)
 CC one or more internal lysine residues or internal lysine analogue residues
 CC for covalent attachment of each of the lipid moieties via the epsilon-
 CC amino group or terminal side-chain group of the lysine or lysine
 CC analogue. Each of the one or more lipid moieties is covalently attached
 CC to an epsilon-amino group of the one or more internal lysine residues or
 CC to a terminal side-chain group of the one or more internal lysine
 CC analogue residues. Also described: (1) producing a lipopeptide; (2) a
 CC composition comprising the lipopeptide and an excipient or diluent; (3)
 CC eliciting an immune response in a subject; (4) immunising a subject
 CC against influenza or hepatitis C virus or Listeria monocytogenes; (5) a
 CC vaccine against an influenza virus or hepatitis C virus or Listeria
 CC monocytogenes comprising the lipopeptides, where the CTL epitope is from
 CC an influenza virus or hepatitis C virus or Listeria monocytogenes protein
 CC ; (6) treating or preventing cancer; and (7) a vaccine against cancer
 CC comprising the lipopeptide, where the CTL epitope is a tumour-specific
 CC CTL epitope. The lipopeptide has cytostatic and virucide activities, and
 CC can be used in vaccine. The lipopeptide is useful for preparing a
 CC composition for treating or preventing cancer, or hepatitis C virus or
 CC influenza virus. The present sequence is used in the exemplification of
 CC the present invention.

XX Sequence 9 AA;

Query Match 89.4%; Score 42; DB 8; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 Db 1 DLMGYIPLV 9

RESULT 38

ID ADO24206 standard; peptide; 9 AA.

XX ADO24206;

XX 01-JUL-2004 (first entry)

XX HCV epitope peptide #5 for multi-epitope construct.

DE hepatotropic; virucide; antiinflammatory; anti-HIV; cytostatic; epitope;
 XX cytotoxic T lymphocyte; CTL; helper T lymphocyte; HTL; immune response;
 KW hepatitis B virus; HBV; HIV; cancer; lymphoma.

XX Hepatitis C virus.

XX WO2004031210-A2.

XX 15-APR-2004.

XX 03-OCT-2003; 2003WO-US031303.

XX 03-OCT-2002; 2002US-0415463P.

XX 22-OCT-2002; 2002US-0419973P.

XX (EPIM-) EPIIMUNE INC.

XX (GEMV) GENENCOR INT. INC.

XX Sette A, Chesnut R, Newman MJ, Livingston BD, Babe LM, Chen Y;

XX Deyoung LM, Huang MTF, Power SD;

XX WPI; 2004-330143/30.

XX New multi-epitope polynucleotides encoding cytotoxic T lymphocyte and/or
 PT helper T lymphocyte epitopes, useful for inducing or stimulating an
 PT antiviral or anticancer immune response, especially against hepatitis B

Best Local Similarity 88.9%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
| | | | |
Db 1 DLMGYIPLV 9

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